

SEQUENCE LISTING

5 (2) INFORMATION FOR SEQ ID NO:1: MTB32A (Ra35 FL)

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 1872 base pairs
(B) TYPE: nucleic acid
10 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```

15 GACTACGTTG GTGTAGAAAA ATCCTGCCGC CCGGACCCTT AAGGCTGGGA CAATTTCTGA      60
   TAGCTACCCC GACACAGGAG GTTACGGGAT GAGCAATTCG CGCCGCCGCT CACTCAGGTG      120
   GTCATGGTTG CTGAGCGTGC TGGCTGCCGT CGGGCTGGGC CTGGCCACGG CGCCGGCCCA      180
   GGCGGCCCCG CCGGCTTGT CGCAGGACCG GTTCGCCGAC TTCCCCGCGC TGCCCCCTCGA      240
   CCCGTCCGCG ATGGTCGCCC AAGTGGCGCC ACAGGTGGTC AACATCAACA CCAAAGTGGG      300
20 CTACAACAAC GCCGTGGGCG CCGGGACCGG CATCGTCATC GATCCCAACG GTGTCTGTCT      360
   GACCAACAAC CACGTGATCG CCGGCGCCAC CGACATCAAT GCGTTCAGCG TCGGCTCCGG      420
   CCAAACCTAC GGCCTCGATG TGGTCGGGTA TGACCGCACC CAGGATGTCT CGGTGCTGCA      480
   GCTGCGCGGT GCCGTGGGCC TGCCGTCCGC GGCATCGGT GCGGCGCTCG CGGTTGGTGA      540
   GCCCGTCGTC GCGATGGGCA ACAGCGGTGG GCAGGGCGGA ACGCCCCGTG CGGTGCCTGG      600
25 CAGGGTGGTC GCGCTCGGCC AAACCGTGCA GCGCTCGGAT TCGTGACCG GTGCCGAAGA      660
   GACATTGAAC GGGTTGATCC AGTTCGATGC CGCAATCCAG CCCGGTGATT CGGGCGGGCC      720
   CGTCGTCAAC GGCCTAGGAC AGGTGGTCGG TATGAACACG GCCCGGTCCG ATAACTTCCA      780
   GCTGTCCAG GGTGGGCAGG GATTCCGCAT TCCGATCGGG CAGGCGATGG CGATCGCGGG      840
   CCAAAATCCGA TCGGTGGGG GGTACCCAC CGTTCATATC GGGCCTACCG CCTTCCTCGG      900
30 CTTGGGTGTT GTCGACAACA ACGGCAACGG CGCAGAGTC CAACGCGTGG TCGGAAGCGC      960
   TCCGGCGGCA AGTCTCGGCA TCTCCACCGG CGACGTGATC ACCGCGGTCT ACGGCGCTCC      1020
   GATCAACTCG GCCACCGCGA TGGCGGACGC GCTTAACGGG CATCATCCCG GTGACGTCTAT      1080
   CTCGGTGAAC TGGCAAACCA AGTCGGGCGG CACGCGTACA GGGAACGTGA CATTGGCCGA      1140
   GGGACCCCG GCCTGATTTG TCGCGGATAC CACCCGCCCG CCGGCCAATT GGATTGGCGC      1200
35 CAGCCGTGAT TGCCCGGTGA GCCCCGAGT TCCGTCTCCC GTGCGCGTGG CATTGTGGAA      1260
   GCAATGAACG AGGCAGAACA CAGCGTTGAG CACCCTCCCG TGCAGGGCAG TTACGTCGAA      1320
   GGCGGTGTGG TCGAGCATCC GGATGCCAAG GACTTCGGCA GCGCCGCCGC CCTGCCCGCC      1380
   GATCCGACCT GGTTTAAGCA CGCCGTCTTC TACGAGGTGC TGGTCCGGGC GTTCTTCGAC      1440
   GCCAGCGCGG ACGGTTCCGN CGATCTGCGT GGACTCATCG ATCGCTCGA CTACCTGCAG      1500
40 TGGCTTGGCA TCGACTGCAT CTGTTGCCGC GTTCCTACG ACTACCGCT GCGCGACGGC      1560
   GGTTACGACA TTCGCGACTT CTACAAGTG CTGCCCCAAT TCGGCACCGT CGACGATTTC      1620
   GTCGCCCTGG TCGACACCGC TCACCGCGCA GGTATCCGCA TCATCACCGA CCTGGTGATG      1680
   AATCACACCT CGGAGTCGCA CCCCTGGTTT CAGGAGTCCC GCGCGACCC AGACGGACCG      1740
   TACGGTGAAT ATTACGTGTG GAGCGACACC AGCGAGCGCT ACACCGACGC CCGGATCATC      1800
45 TTCGTCGACA CCGAAGAGTC GAACTGGTCA TTGATCCTG TCCGCCGACA GTTNCTACTG      1860
   GCACCGATTTC TT
1872

```

(2) INFORMATION FOR SEQ ID NO:2:

(i) SEQUENCE CHARACTERISTICS:

- (A) LENGTH: 355 amino acids
(B) TYPE: amino acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:2: MTB32A (Ra35FL)

```

60 Met Ser Asn Ser Arg Arg Arg Ser Leu Arg Trp Ser Trp Leu Leu Ser
   1           5           10           15
   Val Leu Ala Ala Val Gly Leu Gly Leu Ala Thr Ala Pro Ala Gln Ala
   20           25           30
   Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
   35           40           45
65 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
   50           55           60
   Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
   65           70           75           80

```

5 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
85 90 95
Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
100 105 110
Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
115 120 125
Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
130 135 140
10 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
145 150 155 160
Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
165 170 175
Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
180 185 190
15 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser
195 200 205
Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
210 215 220
20 Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe Ala
225 230 235 240
Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser Gly
245 250 255
Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly Leu
260 265 270
25 Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val Val
275 280 285
Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val Ile
290 295 300
30 Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala Asp
305 310 315 320
Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp Gln
325 330 335
Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu Gly
340 345 350
35 Pro Pro Ala
355

40 <212> DNA
<213> Ra35 mature
<400> SEQ ID NO:3

45 catatgcatc accatcacca tcacgccccg ccggccttgt cgcaggaccg gttcgccgac 60
ttccccgcgc tgccccctcga cccgtccgcg atggtcgccc aagtggggcc acaggtggtc 120
aacatcaaca ccaaactggg ctacaacaac gccgtgggcg ccgggaccgg catcgtcac 180
gatcccaacg gtgtcgtgct gaccaacaac cacgtgatcg cgggcgccac cgacatcaat 240
gcgttcagcg tcggctccgg ccaaacttac gggtcgatg tggtcgggta tgaccgcacc 300
caggatgtcg cgggtgctgca gctgcgcggt gccggtggcc tgccgtcggc ggcgatcgg 360
ggcggcgctc cgggttggtga gccgcgtcgtc gcgatgggca acagcgggtg gcaggggcga 420
50 acgccccgtg cgggtgcctgg cagggtgggtc gcgctcgccc aaaccgtgca ggcgtcggat 480
tcgctgaccg gtgccgaaga gacattgaac gggttgatcc agttcgatgc cgcgatccag 540
cccggtgagg cgggcggggc cgtcgtcaac ggccataggc aggtgggtcgg tatgaacacg 600
gccgcgtccg ataacttcca gctgtcccag ggtgggcagg gattcgccat tccgatcggg 660
caggcgatgg cgatecgcggg ccagatccga tcgggtgggg ggtcaccac cgttcatatc 720
55 gggcctaccg ccttctcctg cttgggtggt gtcgacaaca acggcaacgg cgcacgagtc 780
caacgcgtgg tcgggagcgc tccggcgcca agtctcggca tctccaccgg cgacgtgatc 840
accgcggtcg acgggcgtcc gatcaactcg gccaccgcga tggcggacgc gcttaacggg 900
catcatcccg gtgacgtcat ctccggtgacc tggcaaacca agtcggggcg caccggtaca 960
60 gggaacgtga cattggccga gggacccccg gcctgagaat tc 1002

65 <212> PRT
<213> Ra35 mature
<400> SEQ ID NO:4

Met His His His His His His Ala Pro Pro Ala Leu Ser Gln Asp Arg
5 10 15

Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
 20 25 30
 5 Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
 35 40 45
 Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
 50 55 60
 10 Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
 65 70 75 80
 Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
 85 90 95
 15 Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
 100 105 110
 20 Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val
 115 120 125
 Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
 130 135 140
 25 Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
 145 150 155 160
 Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
 165 170 175
 30 Ala Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly
 180 185 190
 35 Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
 195 200 205
 Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
 210 215 220
 40 Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly
 225 230 235 240
 Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
 245 250 255
 45 Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
 260 265 270
 50 Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
 275 280 285
 Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
 290 295 300
 55 Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
 305 310 315 320
 Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 325 330
 60

<212> DNA
 <213> Ra35FLMutSA
 <400> SEQ ID NO:5
 65 catatgcatc accatcacca tcacgccccg ccggccttgt cgcaggaccg gttcgccgac 60
 ttccccgcgc tgccccctcga cccgtccgcg atggtcgccc aagtggggcc acaggtggtc 120
 aacatcaaca ccaaactggg ctacaacaac gccgtgggcg ccgggaccg catcgatc 180

```

gatcccaacg gtgtcgtgct gaccaacaac cacgtgatcg cgggcgccac cgacatcaat 240
gcgttcagcg tcgggtcccg ccaaacctac ggcgtcgatg tggtcgggta tgaccgcacc 300
caggatgtcg cgggtgctgca gctgcgcggt gccggtggcc tgccgtcggc ggcgatcgg 360
ggcggcgctcg cgggttggtga gcccgtcgtc gcgatgggca acagcgggtg gcagggcgga 420
5 acgccccgtg cgggtgcctgg caggggtggtc gcgctcggcc aaaccgtgca ggcgtcggat 480
tcgctgaccg gtgccgaaga gacattgaac gggttgatcc agttcgatgc cgcgatccag 540
cccggtgatg cgggcggggcc cgtcgtcaac ggcctaggac aggtgggtcgg tatgaacacg 600
ggcgcgtccg ataacttcca gctgtcccag ggtgggcagg gattcgccat tccgatcggg 660
10 caggcgatgg cgatcgcggg ccagatccga tcgggtgggg ggtcaccac cgttcataat 720
gggcctaccg ctttctcctgg cttgggtggt gtcgacaaca acggcaacgg cgcacgagtc 780
caacgcgtgg tcgggagcgc tcggcgcgca agtctcggca tctccaccgg cgacgtgatc 840
accgcggtcg acggcgctcc gatcaactcg gccaccgcga tggcggacgc gcttaacggg 900
catcatcccg gtgacgtcat ctcggtgacc tggcaaacca agtcgggcgg cacgcgtaca 960
15 gggaaacgtga cattggccga gggacccccg gcctgagaat tc 1002

```

<212> PRT
 <213> Ra35FLMutSA
 <400> SEQ ID NO:6

```

20 Met His His His His His His Ala Pro Pro Ala Leu Ser Gln Asp Arg
    5 10 15

25 Phe Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala
    20 25 30

    Gln Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn
    35 40 45

30 Asn Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val
    50 55 60

    Val Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala
    65 70 75 80

35 Phe Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr
    85 90 95

    Asp Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly
    100 105 110

    Leu Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val
    115 120 125

45 Val Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val
    130 135 140

    Pro Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser
    145 150 155 160

50 Leu Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala
    165 170 175

    Ala Ile Gln Pro Gly Asp Ala Gly Gly Pro Val Val Asn Gly Leu Gly
    180 185 190

    Gln Val Val Gly Met Asn Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser
    195 200 205

60 Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile
    210 215 220

    Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly
    225 230 235 240

65 Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly
    245 250 255

```

Ala Arg Val Gln Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly
 260 265 270
 5 Ile Ser Thr Gly Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn
 275 280 285
 Ser Ala Thr Ala Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp
 290 295 300
 10 Val Ile Ser Val Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly
 305 310 315 320
 Asn Val Thr Leu Ala Glu Gly Pro Pro Ala
 325 330
 15

(2) INFORMATION FOR SEQ ID NO:7: Ra35 (MTB32A N-term)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 615 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

gccccgcggccttgctgcaggaccgggttcgccgacttccccgcgctgcccctcgaccgctccgcg
 atggctcgcccaagtggggccacaggtgggtcaacatcaacaccaaactgggctacaacaacgcgctg
 30 ggcgcgggaccggcatcgatcatcgatcccaacgggtgctgctgaccaacaaccacgtgatcgcg
 ggccgacacatcaatgcggttcagcgctcggtcccgccaaacctacggcgctcgatgtggctcggg
 tatgaccgcacccaggatgtcgcggtgctgcagctgcgcggtgcccgtggcctgcccgtcggcggcg
 atcgggtggcggcgctgcgggttggtgagcccgctcgctcgcgatgggcaacagcgggtgggcaggcgga
 acgccccgtgcgggtgcccagggtgggtcgcgctcgcccaaaccgtgcaggcgctcggattcgctg
 35 accggtgcccgaagagacattgaacgggttgatccagttcgatgccgcgatccagcccggtagggcg
 ggccgggccgctcgtaacaggcctaggacaggtggctcggtatgaacacggccgcgctcc

(2) INFORMATION FOR SEQ ID NO:8: Ra35 (MTB32A N-term)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 205 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala Leu
 50 Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Ala Pro Gln Val Val
 Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly Thr
 55 Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His Val
 Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly Gln
 Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val Ala
 60 Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile Gly
 Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser Gly
 Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala Leu
 65 Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu Thr
 Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp Ser

Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn Thr
Ala Ala Ser

5

(2) INFORMATION FOR SEQ ID NO:9: Ra12

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 447 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

CGGTATGAAC ACGGCCGCGT CCGATAACTT CCAGCTGTCC CAGGGTGGGC AGGGATTTCG 60
CATTCGGATC GGGCAGGCGA TGGCGATCGC GGGCCAGATC CGATCGGGTG GGGGGTCACC 120
CACCGTTCAT ATCGGGCCTA CCGCCTTCCT CGGCTTGGGT GTTGTCGACA ACAACGGCAA 180
CGGCGCACGA GTCCAACGCG TGGTCGGGAG CGCTCCGGCG GCAAGTCTCG GCATCTCCAC 240
CGGCGACGTG ATCACC GCGG TCGACGGCGC TCCGATCAAC TCGGCCACCG CGATGGCGGA 300
CGCGCTTAAC GGGCATCATC CCGGTGACGT CATCTCGGTG AACTGGCAA CCAAGTCGGG 360
CGGCACGCGT ACAGGGAACG TGACATTGGC CGAGGGACCC CCGGCCTGAT TTCGTCGYGG 420
ATACCACCCG CCGGCCGGCC AATTGGA 447

25

(2) INFORMATION FOR SEQ ID NO:10: Ra12

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 132 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln Gly Phe
1 5 10 15
Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile Arg Ser
20 25 30
Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe Leu Gly
35 40 45
Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln Arg Val
50 55 60
Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly Asp Val
65 70 75 80
Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala Met Ala
85 90 95
Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val Asn Trp
100 105 110
Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu Ala Glu
115 120 125
Gly Pro Pro Ala
130

55

(2) INFORMATION FOR SEQ ID NO:11: TbH9

- (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 851 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

CTGCAGGGTG GCGTGGATGA GCGTCACCGC GGGGCAGGCC GAGCTGACCG CCGCCCAGGT 60
CCGGTTTGCT GCGGCGGCCT ACGAGACGGC GTATGGGCTG ACGGTGCCCC CGCCGGTGAT 120

CGCCGAGAAC CGTGCTGAAC TGATGATTCT GATAGCGACC AACCTCTTGG GGCAAAACAC 180
 CCCGGCGATC GCGGTCAACG AGGCCGAATA CGGCGAGATG TGGGCCCAAG ACGCCGCCGC 240
 GATGTTTGGC TACGCCGCGG CGACGGCGAC GGCGACGGCG ACGTTGCTGC CGTTCGAGGA 300
 5 GGCGCCGGAG ATGACCAGCG CGGGTGGGCT CCTCGAGCAG GCCGCCGCGG TCGAGGAGGC 360
 CTCCGACACC GCCGCGGCGA ACCAGTTGAT GAACAATGTG CCCCAGGCGC TGAACAGTT 420
 GGCCAGCCC ACGCAGGGCA CCACGCCTTC TTCCAAGCTG GGTGGCCTGT GGAAGACGGT 480
 CTCGCCGCAT CGGTCGCCGA TCAGCAACAT GGTGTCGATG GCCAACAACC ACATGTCGAT 540
 GACCAACTCG GGTGTGTCGA TGACCAACAC CTTGAGCTCG ATGTTGAAGG GCTTTGCTCC 600
 GGCGCGGGCC GCCCAGGCCG TGCAAACCGC GGCGCAAAAC GGGGTCCGGG CGATGAGCTC 660
 10 GCTGGGCAGC TCGCTGGGTT CTTGCGGTCT GGGCGGTGGG GTGGCCGCCA ACTTGGGTCG 720
 GGCGGCCTCG GTACGGTATG GTCACCGGGA TGGCGGAAAA TATGCANAGT CTGGTCGGCG 780
 GAACGGTGGT CCGGCGTAAG GTTTACCCCC GTTTTCTGGA TCGGTGAAC TTCGTCAACG 840
 GAAACAGTTA C 851

15

(2) INFORMATION FOR SEQ ID NO:12:

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 263 amino acids
 20 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:12: TbH9

25

Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala Ala
 1 5 10 15
 Gln Val Arg Val Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu Thr
 20 25 30
 30 Val Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile Leu
 35 40 45
 Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val Asn
 50 55 60
 35 Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met Phe
 65 70 75 80
 Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Leu Leu Pro Phe
 85 90 95
 Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln Ala
 100 105 110
 40 Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu Met
 115 120 125
 Asn Asn Val Pro Gln Ala Leu Lys Gln Leu Ala Gln Pro Thr Gln Gly
 130 135 140
 45 Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser Pro
 145 150 155 160
 His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His Met
 165 170 175
 Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser Met
 180 185 190
 50 Leu Lys Gly Phe Ala Pro Ala Ala Ala Gln Ala Val Gln Thr Ala
 195 200 205
 Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu Gly
 210 215 220
 55 Ser Ser Gly Leu Gly Gly Val Ala Ala Asn Leu Gly Arg Ala Ala
 225 230 235 240
 Ser Val Arg Tyr Gly His Arg Asp Gly Gly Lys Tyr Ala Xaa Ser Gly
 245 250 255
 Arg Arg Asn Gly Gly Pro Ala
 260

60

(2) INFORMATION FOR SEQ ID NO:13: TBH9FL

(i) SEQUENCE CHARACTERISTICS:
 65 (A) LENGTH: 3058 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

5	GATCGTACCC GTGCGAGTGC TCGGGCCGTT TGAGGATGGA GTGCACGTGT CTTTCGTGAT	60
	GGCATACCCA GAGATGTTGG CGGCGGCGGC TGACACCCTG CAGAGCATCG GTGCTACCAC	120
	TGTGGCTAGC AATGCCGCTG CGGCGGCCCC GACGACTGGG GTGGTGCCCC CCGCTGCCGA	180
10	TGAGGTGTCG GCGCTGACTG CGGCGCACTT CGCCGCACAT GCGGCGATGT ATCAGTCCGT	240
	GAGCGCTCGG GCTGCTGCGA TTCATGACCA GTTCGTGGCC ACCCTTGCCA GCAGCGCCAG	300
15	CTCGTATGCG GCCACTGAAG TCGCCAATGC GCGGCGGCC AGCTAAGCCA GGAACAGTCG	360
	GCACGAGAAA CCACGAGAAA TAGGGACACG TAATGGTGGA TTTCGGGGCG TTACCACCGG	420
	AGATCAACTC CGCGAGGATG TACGCCGGCC CGGGTTCGGC CTCGCTGGTG GCCGCGGCTC	480
20	AGATGTGGGA CAGCGTGGCG AGTGACCTGT TTTCGGCCGC GTCGGCGTTT CAGTCGGTGG	540
	TCTGGGTCT GACGGTGGGG TCGTGATAG GTTCGTCGGC GGGTCTGATG GTGGCGGCGG	600
25	CCTCGCCGTA TGTGGCGTGG ATGAGCGTCA CCGCGGGGCA GGCCGAGCTG ACCGCCGCC	660
	AGGTCCGGGT TGCTGCGGCG GCCTACGAGA CGGCGTATGG GCTGACGGTG CCCCCGCCG	720
	TGATCGCCGA GAACCGTGCT GAACTGATGA TTCTGATAGC GACCAACCTC TTGGGGCAAA	780
30	ACACCCCGGC GATCGCGGTC AACGAGGCCG AATACGGCGA GATGTGGGCC CAAGACGCCG	840
	CCGCGATGTT TGGCTACGCC GCGCGACGG CGACGGCGAC GCGGACGTTG CTGCCGTTCC	900
35	AGGAGGCGCC GGAGATGACC AGCGCGGGTG GGCTCCTCGA GCAGGCCGCC GCGGTCGAGG	960
	AGGCCTCCGA CACCGCCGCG GCGAACCAGT TGATGAACAA TGTGCCCCAG GCGCTGCAAC	1020
	AGCTGGCCCA GCCACGCAG GGCACCACGC CTTCTTCCAA GCTGGGTGGC CTGTGGAAGA	1080
40	CGGTCTCGCC GCATCGGTCG CCGATCAGCA ACATGGTGTC GATGGCCAA CACCACATGT	1140
	CGATGACCAA CTCGGGTGTG TCGATGACCA ACACCTTGAG CTCGATGTTG AAGGGCTTTG	1200
45	CTCCGGCGGC GGCCGCCAG GCCGTGCAAA CCGCGGCGCA AAACGGGGTC CGGGCGATGA	1260
	GCTCGCTGGG CAGCTCGCTG GGTCTTTCGG GTCTGGGCGG TGGGTGGCC GCCAACTTGG	1320
	GTCGGGCGGC CTCGGTCGGT TCGTTGTTCG TGCCGCAGGC CTGGGCCGCG GCCAACCAGG	1380
50	CAGTCACCCC GCGGCGCGG GCGCTGCCGC TGACCAGCCT GACCAGCGCC GCGGAAAGAG	1440
	GGCCCGGGCA GATGCTGGGC GGGCTGCCGG TGGGGCAGAT GGGCGCCAGG GCCGCTGGTG	1500
55	GGCTCAGTGG TGTGCTGCGT GTTCCGCCGC GACCCTATGT GATGCCGCAT TCTCCGGCGG	1560
	CCGGCTAGGA GAGGGGCGC AGACTGTCGT TATTTGACCA GTGATCGGCG GTCTCGGTGT	1620
	TTCCGCGGCC GGCTATGACA ACAGTCAATG TGCATGACAA GTTACAGGTA TTAGGTCCAG	1680
60	GTTCAACAAG GAGACAGGCA ACATGGCCTC ACGTTTTATG ACGGATCCGC ACGCGATGCG	1740
	GGACATGGCG GGCCGTTTGG AGGTGCACGC CCAGACGGTG GAGGACGAGG CTCGCCGGAT	1800
65	GTGGGCGTCC GCGCAAAACA TTTCGGGTGC GGGCTGGAGT GGCATGGCCG AGGCGACCTC	1860
	GCTAGACACC ATGGCCCAGA TGAATCAGGC GTTTCGCAAC ATCGTGAACA TGCTGCACGG	1920
	GGTGCGTGAC GGGCTGGTTC GCGACGCCAA CAACTACGAG CAGCAAGAGC AGGCCTCCCA	1980

GCAGATCCTC AGCAGCTAAC GTCAGCCGCT GCAGCACAAT ACTTTTACAA GCGAAGGAGA 2040
 5 ACAGGTTCTGA TGACCATCAA CTATCAATTC GGGGATGTCG ACGCTCACGG CGCCATGATC 2100
 CGCGCTCAGG CCGGGTTGCT GGAGGCCGAG CATCAGGCCA TCATTCTGTA TGTGTTGACC 2160
 GCGAGTGACT TTTGGGGCGG CGCCGGTTCG GCGGCCTGCC AGGGGTTTCAT TACCCAGTTG 2220
 10 GGCCGTAAC TCCAGGTGAT CTACGAGCAG GCCAACGCCC ACGGGCAGAA GGTGCAGGCT 2280
 GCCGGCAACA ACATGGCGCA AACCGACAGC GCCGTCGGCT CCAGCTGGGC CTGACACCAG 2340
 15 GCCAAGGCCA GGGACGTGGT GTACGAGTGA AGTTCCTCGC GTGATCCTTC GGGTGGCAGT 2400
 CTAAGTGGTC AGTGCTGGGG TGTGTTGGT TTGCTGCTTG GCGGGTTCTT CCGTGCTGGT 2460
 CAGTGCTGCT CGGGCTCGGG TGAGGACCTC GAGGCCCAGG TAGCGCCGTC CTTGATCCA 2520
 20 TTCGTCGTGT TGTTCGGCGA GGACGGCTCC GACGAGGCGG ATGATCGAGG CGCGGTCGGG 2580
 GAAGATGCCC ACGACGTCGG TTCGGCGTCG TACCTCTCGG TTGAGGCGTT CCTGGGGGTT 2640
 25 GTTGACCAG ATTTGGCGCC AGATCTGCTT GGGGAAGGCG GTGAACGCCA GCAGGTCGGT 2700
 GCGGGCGGTG TCGAGGTGCT CGGCCACCGC GGGGAGTTTG TCGGTCAGAG CGTCGAGTAC 2760
 CCGATCATAT TGGGCAACAA CTGATTCGGC GTCGGGCTGG TCGTAGATGG AGTGCAGCAG 2820
 30 GGTGCGCACC CACGGCCAGG AGGGCTTCGG GGTGGCTGCC ATCAGATTGG CTGCGTAGTG 2880
 GGTCTGTCAG CGCTGCCAGG CCGCTGCGGG CAGGGTGGCG CCGATCGCGG CCACCAGGCC 2940
 GGCGTGGGCG TCGCTGGTGA CCAGCGCGAC CCCGACAGG CCGCGGGCGA CCAGGTCGCG 3000
 35 GAAGAACGCC AGCCAGCCGG CCCCGTCCTC GGCGGAGGTG ACCTGGATGC CCAGGATC 3058

(2) INFORMATION FOR SEQ ID NO:14: TbH9FL

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 391 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

Met Val Asp Phe Gly Ala Leu Pro Pro Glu Ile Asn Ser Ala Arg Met
 1 5 10 15
 Tyr Ala Gly Pro Gly Ser Ala Ser Leu Val Ala Ala Ala Gln Met Trp
 20 25 30
 55 Asp Ser Val Ala Ser Asp Leu Phe Ser Ala Ala Ser Ala Phe Gln Ser
 35 40 45
 Val Val Trp Gly Leu Thr Val Gly Ser Trp Ile Gly Ser Ser Ala Gly
 50 55 60
 60 Leu Met Val Ala Ala Ala Ser Pro Tyr Val Ala Trp Met Ser Val Thr
 65 70 75 80
 65 Ala Gly Gln Ala Glu Leu Thr Ala Ala Gln Val Arg Val Ala Ala Ala
 85 90 95
 Ala Tyr Glu Thr Ala Tyr Gly Leu Thr Val Pro Pro Pro Val Ile Ala
 100 105 110

Glu Asn Arg Ala Glu Leu Met Ile Leu Ile Ala Thr Asn Leu Leu Gly
 115 120 125
 5 Gln Asn Thr Pro Ala Ile Ala Val Asn Glu Ala Glu Tyr Gly Glu Met
 130 135 140
 Trp Ala Gln Asp Ala Ala Ala Met Phe Gly Tyr Ala Ala Ala Thr Ala
 145 150 155 160
 10 Thr Ala Thr Ala Thr Leu Leu Pro Phe Glu Glu Ala Pro Glu Met Thr
 165 170 175
 Ser Ala Gly Gly Leu Leu Glu Gln Ala Ala Ala Val Glu Glu Ala Ser
 180 185 190
 15 Asp Thr Ala Ala Ala Asn Gln Leu Met Asn Asn Val Pro Gln Ala Leu
 195 200 205
 20 Gln Gln Leu Ala Gln Pro Thr Gln Gly Thr Thr Pro Ser Ser Lys Leu
 210 215 220
 Gly Gly Leu Trp Lys Thr Val Ser Pro His Arg Ser Pro Ile Ser Asn
 225 230 235 240
 25 Met Val Ser Met Ala Asn Asn His Met Ser Met Thr Asn Ser Gly Val
 245 250 255
 Ser Met Thr Asn Thr Leu Ser Ser Met Leu Lys Gly Phe Ala Pro Ala
 260 265 270
 Ala Ala Ala Gln Ala Val Gln Thr Ala Ala Gln Asn Gly Val Arg Ala
 275 280 285
 35 Met Ser Ser Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly
 290 295 300
 Val Ala Ala Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val
 305 310 315 320
 40 Pro Gln Ala Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg
 325 330 335
 Ala Leu Pro Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly
 340 345 350
 Gln Met Leu Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly
 355 360 365
 50 Gly Gly Leu Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met
 370 375 380
 Pro His Ser Pro Ala Ala Gly
 385 390

55

<210> SEQ ID NO:15

<211> 2287

<212> DNA

60

<213> Artificial Sequence

<223> Description of Artificial Sequence:tri-fusion
 protein Mtb72F(Ra12-TbH9-Ra35 or Mtb32-Mtb39
 fusion)

65

tctagaaata attttgttta ctttaagaan ganatataca t atg cat cac cat cac 56
 Met His His His His
 1 5

	cat cac acg gcc gcg tcc gat aac ttc cag ctg tcc cag ggt ggg cag	104
	His His Thr Ala Ala Ser Asp Asn Phe Gln Leu Ser Gln Gly Gly Gln	
	10 15 20	
5	gga ttc gcc att ccg atc ggg cag gcg atg gcg atc gcg ggc cag atc	152
	Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala Ile Ala Gly Gln Ile	
	25 30 35	
10	cga tcg ggt ggg ggg tca ccc acc gtt cat atc ggg cct acc gcc ttc	200
	Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile Gly Pro Thr Ala Phe	
	40 45 50	
15	ctc ggc ttg ggt gtt gtc gac aac aac ggc aac ggc gca cga gtc caa	248
	Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn Gly Ala Arg Val Gln	
	55 60 65	
20	cgc gtg gtc ggg agc gct ccg gcg gca agt ctc ggc atc tcc acc ggc	296
	Arg Val Val Gly Ser Ala Pro Ala Ala Ser Leu Gly Ile Ser Thr Gly	
	70 75 80 85	
25	gac gtg atc acc gcg gtc gac ggc gct ccg atc aac tcg gcc acc gcg	344
	Asp Val Ile Thr Ala Val Asp Gly Ala Pro Ile Asn Ser Ala Thr Ala	
	90 95 100	
30	atg gcg gac gcg ctt aac ggg cat cat ccc ggt gac gtc atc tcg gtg	392
	Met Ala Asp Ala Leu Asn Gly His His Pro Gly Asp Val Ile Ser Val	
	105 110 115	
35	acc tgg caa acc aag tcg ggc ggc acg cgt aca ggg aac gtg aca ttg	440
	Thr Trp Gln Thr Lys Ser Gly Gly Thr Arg Thr Gly Asn Val Thr Leu	
	120 125 130	
40	gcc gag gga ccc ccg gcc gaa ttc atg gtg gat ttc ggg gcg tta cca	488
	Ala Glu Gly Pro Pro Ala Glu Phe Met Val Asp Phe Gly Ala Leu Pro	
	135 140 145	
45	ccg gag atc aac tcc gcg agg atg tac gcc ggc ccg ggt tcg gcc tcg	536
	Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser	
	150 155 160 165	
50	ctg gtg gcc gcg gct cag atg tgg gac agc gtg gcg agt gac ctg ttt	584
	Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe	
	170 175 180	
55	tcg gcc gcg tcg gcg ttt cag tcg gtg gtc tgg ggt ctg acg gtg ggg	632
	Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly	
	185 190 195	
60	tcg tgg ata ggt tcg tcg gcg ggt ctg atg gtg gcg gcg gcc tcg ccg	680
	Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ser Pro	
	200 205 210	
65	tat gtg gcg tgg atg agc gtc acc gcg ggg cag gcc gag ctg acc gcc	728
	Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala	
	215 220 225	
70	gcc cag gtc ccg gtt gct gcg gcg gcc tac gag acg gcg tat ggg ctg	776
	Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu	
	230 235 240 245	
75	acg gtg ccc ccg ccg gtg atc gcc gag aac cgt gct gaa ctg atg att	824
	Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile	
	250 255 260	
80	ctg ata gcg acc aac ctc ttg ggg caa aac acc ccg gcg atc gcg gtc	872
	Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val	
	265 270 275	

	aac Asn	gag Glu	gcc Ala	gaa Glu	tac Tyr	ggc Gly	gag Glu	atg Met	tgg Trp	gcc Ala	caa Gln	gac Asp	gcc Ala	gcc Ala	gcg Ala	atg Met	920
			280					285				290					
5	ttt Phe	ggc Gly	tac Tyr	gcc Ala	gcg Ala	gcg Ala	acg Thr	gcg Ala	acg Thr	gcg Ala	acg Thr	gcg Ala	acg Thr	ttg Leu	ctg Leu	cgc Pro	968
		295					300					305					
10	ttc Phe	gag Glu	gag Glu	gcg Ala	ccg Pro	gag Glu	atg Met	acc Thr	agc Ser	gcg Ala	ggc Gly	ggg Gly	ctc Leu	ctc Leu	gag Glu	cag Gln	1016
		310				315					320					325	
15	gcc Ala	gcc Ala	gcg Ala	gtc Val	gag Glu	gag Glu	gcc Ala	tcc Ser	gac Asp	acc Thr	gcc Ala	gcg Ala	gcg Ala	aac Asn	cag Gln	ttg Leu	1064
				330						335					340		
20	atg Met	aac Asn	aat Asn	gtg Val	ccc Pro	cag Gln	gcg Ala	ctg Leu	caa Gln	cag Gln	ctg Leu	gcc Ala	cag Gln	ccc Pro	acg Thr	cag Gln	1112
				345					350					355			
	ggc Gly	acc Thr	acg Thr	cct Pro	tct Ser	tcc Ser	aag Lys	ctg Leu	ggc Gly	ggc Gly	ctg Leu	tgg Trp	aag Lys	acg Thr	gtc Val	tcg Ser	1160
			360					365					370				
25	ccg Pro	cat His	cgg Arg	tcg Ser	ccg Pro	atc Ile	agc Ser	aac Asn	atg Met	gtg Val	tcg Ser	atg Met	gcc Ala	aac Asn	aac Asn	cac His	1208
		375					380					385					
30	atg Met	tcg Ser	atg Met	acc Thr	aac Asn	tcg Ser	ggc Gly	gtg Val	tcg Ser	atg Met	acc Thr	aac Asn	acc Thr	ttg Leu	agc Ser	tcg Ser	1256
		390				395					400					405	
35	atg Met	ttg Leu	aag Lys	ggc Gly	ttt Phe	gct Ala	ccg Pro	gcg Ala	gcg Ala	gcc Ala	cgc Arg	cag Gln	gcc Ala	gtg Val	caa Gln	acc Thr	1304
				410						415					420		
40	gcg Ala	gcg Ala	caa Gln	aac Asn	ggg Gly	gtc Val	ccg Arg	gcg Ala	atg Met	agc Ser	tcg Ser	ctg Leu	ggc Gly	agc Ser	tcg Ser	ctg Leu	1352
				425					430				435				
	ggc Gly	tct Ser	tcg Ser	ggc Gly	ctg Leu	ggc Gly	ggc Gly	gtg Val	gcc Ala	gcc Ala	aac Asn	ttg Leu	ggc Gly	ggc Gly	cgc Arg	gcg Ala	1400
			440				445					450					
45	gcc Ala	tcg Ser	gtc Val	ggc Gly	tcg Ser	ttg Leu	tcg Ser	gtg Val	ccg Pro	cag Gln	gcc Ala	tgg Trp	gcc Ala	gcg Ala	gcc Ala	aac Asn	1448
		455					460					465					
50	cag Gln	gca Ala	gtc Val	acc Thr	ccg Pro	gcg Ala	gcg Ala	ccg Arg	gcg Ala	ctg Leu	ccg Pro	ctg Leu	acc Thr	agc Ser	ctg Leu	acc Thr	1496
		470				475					480					485	
55	agc Ser	gcc Ala	gcg Ala	gaa Glu	aga Arg	ggg Gly	ccc Pro	ggg Gly	cag Gln	atg Met	ctg Leu	ggc Gly	ggg Gly	ctg Leu	ccg Pro	gtg Val	1544
				490					495					500			
	ggg Gly	cag Gln	atg Met	ggc Gly	agg Ala	gcc Arg	ggc Ala	ggc Gly	ggc Gly	ggc Gly	ctc Leu	agt Ser	ggc Gly	gtg Val	ctg Leu	cgt Arg	1592
				505				510					515				
60	gt																

	ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg cca cag gtg	1736
	Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val	
	550 555 560 565	
5	gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg	1784
	Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly	
	570 575 580	
10	acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac	1832
	Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His	
	585 590 595	
15	gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc	1880
	Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly	
	600 605 610	
20	caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc	1928
	Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val	
	615 620 625	
25	gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tcg gcg gcg atc	1976
	Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile	
	630 635 640 645	
30	ggc ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc	2024
	Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser	
	650 655 660	
35	ggc ggc cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg	2072
	Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala	
	665 670 675	
40	ctc ggc caa acc gtg cag gcg tcg gat tcg ctg acc ggt gcc gaa gag	2120
	Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu	
	680 685 690	
45	aca ttg aac ggc ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat	2168
	Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp	
	695 700 705	
50	tcg ggc ggc ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac	2216
	Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn	
	710 715 720 725	
55	acg gcc gcg tcc taggatattcc atcacactgg cggccgctcg agcagatccg	2268
	Thr Ala Ala Ser	
60	gntgtaacaa agcccgaata	2287
55	<210> SEQ ID NO:16 <211> 729 <212> PRT <213> Artificial Sequence <223> Description of Artificial Sequence:tri-fusion protein Mtb72F (Ra12-TbH9-Ra35 or Mtb32-Mtb39 fusion)	
65	Met His His His His His His Thr Ala Ala Ser Asp Asn Phe Gln Leu	
	1 5 10 15	
70	Ser Gln Gly Gly Gln Gly Phe Ala Ile Pro Ile Gly Gln Ala Met Ala	
	20 25 30	
75	Ile Ala Gly Gln Ile Arg Ser Gly Gly Gly Ser Pro Thr Val His Ile	
	35 40 45	
80	Gly Pro Thr Ala Phe Leu Gly Leu Gly Val Val Asp Asn Asn Gly Asn	

	50				55				60							
5	Gly 65	Ala	Arg	Val	Gln	Arg 70	Val	Val	Gly	Ser	Ala 75	Pro	Ala	Ala	Ser	Leu 80
	Gly	Ile	Ser	Thr	Gly 85	Asp	Val	Ile	Thr	Ala 90	Val	Asp	Gly	Ala	Pro 95	Ile
10	Asn	Ser	Ala	Thr 100	Ala	Met	Ala	Asp	Ala 105	Leu	Asn	Gly	His	His 110	Pro	Gly
	Asp	Val	Ile 115	Ser	Val	Thr	Trp	Gln 120	Thr	Lys	Ser	Gly	Gly 125	Thr	Arg	Thr
15	Gly 130	Asn	Val	Thr	Leu	Ala	Glu 135	Gly	Pro	Pro	Ala	Glu 140	Phe	Met	Val	Asp
	Phe 145	Gly	Ala	Leu	Pro	Pro 150	Glu	Ile	Asn	Ser	Ala 155	Arg	Met	Tyr	Ala	Gly 160
20	Pro	Gly	Ser	Ala	Ser 165	Leu	Val	Ala	Ala 170	Ala	Gln	Met	Trp	Asp	Ser 175	Val
25	Ala	Ser	Asp	Leu 180	Phe	Ser	Ala	Ala	Ser 185	Ala	Phe	Gln	Ser	Val 190	Val	Trp
	Gly	Leu	Thr 195	Val	Gly	Ser	Trp	Ile 200	Gly	Ser	Ser	Ala 205	Gly	Leu	Met	Val
30	Ala 210	Ala	Ala	Ser	Pro	Tyr	Val 215	Ala	Trp	Met	Ser	Val 220	Thr	Ala	Gly	Gln
	Ala 225	Glu	Leu	Thr	Ala	Ala 230	Gln	Val	Arg	Val	Ala 235	Ala	Ala	Ala	Tyr	Glu 240
35	Thr	Ala	Tyr	Gly	Leu 245	Thr	Val	Pro	Pro	Pro 250	Val	Ile	Ala	Glu	Asn 255	Arg
	Ala	Glu	Leu	Met 260	Ile	Leu	Ile	Ala	Thr 265	Asn	Leu	Leu	Gly	Gln 270	Asn	Thr
40	Pro	Ala	Ile 275	Ala	Val	Asn	Glu	Ala 280	Glu	Tyr	Gly	Glu 285	Met	Trp	Ala	Gln
45	Asp 290	Ala	Ala	Ala	Met	Phe	Gly 295	Tyr	Ala	Ala	Ala 300	Thr	Ala	Thr	Ala	Thr
	Ala 305	Thr	Leu	Leu	Pro	Phe 310	Glu	Glu	Ala	Pro	Glu 315	Met	Thr	Ser	Ala	Gly 320
50	Gly	Leu	Leu	Glu	Gln 325	Ala	Ala	Ala	Val	Glu 330	Glu	Ala	Ser	Asp	Thr 335	Ala
	Ala	Ala	Asn	Gln 340	Leu	Met	Asn	Asn 345	Val	Pro	Gln	Ala	Leu 350	Gln	Gln	Leu
55	Ala	Gln	Pro 355	Thr	Gln	Gly	Thr	Thr 360	Pro	Ser	Ser	Lys 365	Leu	Gly	Gly	Leu
60	Trp 370	Lys	Thr	Val	Ser	Pro	His 375	Arg	Ser	Pro	Ile 380	Ser	Asn	Met	Val	Ser
	Met 385	Ala	Asn	Asn	His	Met 390	Ser	Met	Thr	Asn	Ser 395	Gly	Val	Ser	Met	Thr 400
65	Asn	Thr	Leu	Ser	Ser 405	Met	Leu	Lys	Gly	Phe 410	Ala	Pro	Ala	Ala	Ala 415	Arg
	Gln	Ala	Val	Gln	Thr	Ala	Ala	Gln	Asn	Gly	Val	Arg	Ala	Met	Ser	Ser

	420	425	430
5	Leu Gly Ser Ser Leu Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala 435 440 445		
	Asn Leu Gly Arg Ala Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala 450 455 460		
10	Trp Ala Ala Ala Asn Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro 465 470 475 480		
	Leu Thr Ser Leu Thr Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu 485 490 495		
15	Gly Gly Leu Pro Val Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu 500 505 510		
	Ser Gly Val Leu Arg Val Pro Pro Arg Pro Tyr Val Met Pro His Ser 515 520 525		
20	Pro Ala Ala Gly Asp Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe 530 535 540		
	Ala Asp Phe Pro Ala Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln 545 550 555 560		
25	Val Gly Pro Gln Val Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn 565 570 575		
30	Ala Val Gly Ala Gly Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val 580 585 590		
	Leu Thr Asn Asn His Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe 595 600 605		
35	Ser Val Gly Ser Gly Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp 610 615 620		
40	Arg Thr Gln Asp Val Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu 625 630 635 640		
	Pro Ser Ala Ala Ile Gly Gly Gly Val Ala Val Gly Glu Pro Val Val 645 650 655		
45	Ala Met Gly Asn Ser Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro 660 665 670		
	Gly Arg Val Val Ala Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu 675 680 685		
50	Thr Gly Ala Glu Glu Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala 690 695 700		
55	Ile Gln Pro Gly Asp Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln 705 710 715 720		
	Val Val Gly Met Asn Thr Ala Ala Ser 725		
60	<210> SEQ ID NO:17 <211> 2190 <212> DNA <213> Mtb72FMutSA		
65	atgcatcacc atcaccatca cacggccgcg tccgataact tccagctgtc ccaggggtggg 60 cagggattcg ccattccgat cgggcaggcg atggcgatcg cgggccagat ccgatcgggt 120 gggggggtcac ccaccgttca tatcgggcct accgccttcc tcggcttggg tggtgtcgac 180		

5	aacaacggca	acggcgcacg	agtccaacgc	gtggtcggga	gcgctccggc	ggcaagtctc	240
	ggcatctcca	ccggcgacgt	gatcaccgcg	gtcgcaggcg	ctccgatcaa	ctcggccacc	300
	gcgatggcgg	acgcgcttaa	cgggcatcat	cccggtgacg	tcattctcgg	gacctggcaa	360
	accaagtctg	gcgcgacgcg	tacagggaac	gtgacattgg	ccgaggggac	cccggccgaa	420
	ttcatggttg	atttcggggc	gttaccacga	cagatcaact	ccgcgaggat	gtacgcggcg	480
10	ccgggtctcg	cctcgctggg	ggccgcggct	cagatgtggg	acagcgtggc	gagtgcacct	540
	ttttcggcgg	cgtcggcggt	tcagtcggtg	gtctgggggt	tgacgggtgg	gtcgtggata	600
	ggttcgtcgg	cgggtctgat	ggtggcggcg	gctcgcgcgt	atgtggcgtg	gatgagcgtc	660
	accgcggggc	aggccgagct	gaccgcgcgc	caggtccggg	ttgctcggcg	ggcctacgag	720
	acggcgctatg	ggctgacggt	gccccgcgcg	gtgatccgcg	agaaccgtgc	tgaactgatg	780
15	attctgatag	cgaccaacct	cttggggcaa	aacaccccg	cgatcgcggt	caacgaggcc	840
	gaatacggcg	agatgtgggc	ccaagacgcc	gccgcgatgt	ttggctacgc	cgcggcgacg	900
	gcgactggcg	cggcgacgtt	gctgccggtt	gaggaggcgc	cggagatgac	cagcgcgggt	960
	gggctcctcg	agcaggcgcg	cgcgctcgag	gaggcctccg	acaccgcgcg	ggcgaaccag	1020
	ttgatgaaca	atgtgcccca	ggcgctgcga	cagctggccc	agccccgcga	gggcaccacg	1080
20	ccttcttcca	agctgggttg	cctgtggaag	acggtctcgc	cgcatacggt	gccgatcagc	1140
	aacatggtgt	cgatggccaa	caaccacatg	tcgatgacca	actcgggtgt	gtcgatgacc	1200
	aacacccttg	gctcgatggt	gaagggcttt	gtccgcggcg	cggccgccca	ggcgtgcaa	1260
	accgcggcgc	aaaacggggg	cggggcgatg	agctcgctgg	gcagctcgct	ttcgttcttcg	1320
	ggctcggggc	gtgggggtgg	cgccaacttg	ggtcggggcg	cctcggctcg	ttcgttgtcg	1380
25	gtgccgcagg	cctggggcgc	ggccaaccag	gcagtcaccc	cggcggcgcg	ggcgtgccc	1440
	ctgaccagcc	tgaccagcgc	cgcggaaaga	gggcccgggc	agatgctggg	cgggctgcgg	1500
	gtggggcaga	tgggcgccag	ggccgggtgt	gggctcagtg	gtgtgctggg	tgttccgcgc	1560
	cgaccctatg	tgatgcgcga	ttctccggca	ggcgcgata	tcgcccgcgc	gccttgtctg	1620
	caggaccggt	tcgcgcactt	cccgcgcgtg	ccctcgacc	cgtccgcgat	ggtcgcccaa	1680
30	gtggggccac	agtggttcaa	catcaacacc	aaactgggct	acaacaacgc	cgtgggcgcc	1740
	gggaccggca	tcgtcatcga	tcccaacggt	gtcgtgctga	ccaacaacca	cgtgatcggt	1800
	ggcgccacgc	acatcaatgc	gttcagcgtc	ggctccggcg	aaacctacgg	cgtcgtatgt	1860
	gtcgggtatg	accgcaccca	ggatgtcgcg	gtgctgcagc	tgccgctgtg	cgttgacctg	1920
	ccgtcggcgg	cgatcggttg	cggcgtcgcg	gttggtgagc	ccgtcgtcgc	gatgggcaac	1980
35	agcgggtggc	aggcggaac	gccccgtcgc	gtgcctggca	gggtggtcgc	gctcggccaa	2040
	accgtgcagg	cgtcggattc	gctgacccgt	gccgaagaga	cattgaacgg	gttgatccag	2100
	ttcgatgcgc	cgatccagcc	cggtagtcgc	ggcggggcgg	tcgtcaacgg	cctaggacag	2160
	qtggtcgqta	tgaacacggc	cgcgtcctag				2190

```
<210> SEQ ID NO:18
<211> 729
<212> PRT
<213> Mtb72FMutSA
```

65

	Phe Gly Ala Leu Pro	Pro Glu Ile Asn Ser	Ala Arg Met Tyr Ala Gly	145	150	155	160
5	Pro Gly Ser Ala Ser	Leu Val Ala Ala Ala	Gln Met Trp Asp Ser Val	165	170	175	
	Ala Ser Asp Leu Phe	Ser Ala Ala Ser	Ala Phe Gln Ser Val Val Trp	180	185	190	
10	Gly Leu Thr Val Gly	Ser Trp Ile Gly Ser Ser	Ala Gly Leu Met Val	195	200	205	
	Ala Ala Ala Ser Pro	Tyr Val Ala Trp Met Ser	Val Thr Ala Gly Gln	210	215	220	
15	Ala Glu Leu Thr Ala	Ala Gln Val Arg Val	Ala Ala Ala Tyr Glu	225	230	235	240
20	Thr Ala Tyr Gly Leu	Thr Val Pro Pro Pro	Val Ile Ala Glu Asn Arg	245	250	255	
	Ala Glu Leu Met Ile	Leu Ile Ala Thr Asn	Leu Leu Gly Gln Asn Thr	260	265	270	
25	Pro Ala Ile Ala Val	Asn Glu Ala Glu Tyr	Gly Glu Met Trp Ala Gln	275	280	285	
	Asp Ala Ala Ala Met	Phe Gly Tyr Ala Ala	Ala Thr Ala Thr Ala Thr	290	295	300	
30	Ala Thr Leu Leu Pro	Phe Glu Glu Ala Pro	Glu Met Thr Ser Ala Gly	305	310	315	320
35	Gly Leu Leu Glu Gln	Ala Ala Ala Val Glu	Glu Ala Ser Asp Thr Ala	325	330	335	
	Ala Ala Asn Gln Leu	Met Asn Asn Val Pro	Gln Ala Leu Gln Gln Leu	340	345	350	
40	Ala Gln Pro Thr Gln	Gly Thr Thr Pro Ser	Ser Lys Leu Gly Gly Leu	355	360	365	
	Trp Lys Thr Val Ser	Pro His Arg Ser Pro	Ile Ser Asn Met Val Ser	370	375	380	
45	Met Ala Asn Asn His	Met Ser Met Thr Asn	Ser Gly Val Ser Met Thr	385	390	395	400
50	Asn Thr Leu Ser Ser	Met Leu Lys Gly Phe	Ala Pro Ala Ala Ala Ala	405	410	415	
	Gln Ala Val Gln Thr	Ala Ala Gln Asn Gly	Val Arg Ala Met Ser Ser	420	425	430	
55	Leu Gly Ser Ser Leu	Gly Ser Ser Gly Leu	Gly Gly Val Ala Ala	435	440	445	
	Asn Leu Gly Arg Ala	Ala Ala Ser Val Gly	Ser Leu Ser Val Pro Gln Ala	450	455	460	
60	Trp Ala Ala Ala Asn	Gln Ala Val Thr Pro	Ala Ala Arg Ala Leu Pro	465	470	475	480
65	Leu Thr Ser Leu Thr	Ser Ala Ala Glu Arg	Gly Pro Gly Gln Met Leu	485	490	495	
	Gly Gly Leu Pro Val	Gly Gln Met Gly Ala	Arg Ala Gly Gly Gly Leu	500	505	510	

	Ser	Gly	Val	Leu	Arg	Val	Pro	Pro	Arg	Pro	Tyr	Val	Met	Pro	His	Ser			
			515						520				525						
5	Pro	Ala	Ala	Gly	Asp	Ile	Ala	Pro	Pro	Ala	Leu	Ser	Gln	Asp	Arg	Phe			
		530					535					540							
	Ala	Asp	Phe	Pro	Ala	Leu	Pro	Leu	Asp	Pro	Ser	Ala	Met	Val	Ala	Gln			
10		545				550					555					560			
	Val	Gly	Pro	Gln	Val	Val	Asn	Ile	Asn	Thr	Lys	Leu	Gly	Tyr	Asn	Asn			
					565					570					575				
	Ala	Val	Gly	Ala	Gly	Thr	Gly	Ile	Val	Ile	Asp	Pro	Asn	Gly	Val	Val			
15				580					585					590					
	Leu	Thr	Asn	Asn	His	Val	Ile	Ala	Gly	Ala	Thr	Asp	Ile	Asn	Ala	Phe			
			595					600					605						
20	Ser	Val	Gly	Ser	Gly	Gln	Thr	Tyr	Gly	Val	Asp	Val	Val	Gly	Tyr	Asp			
		610					615					620							
	Arg	Thr	Gln	Asp	Val	Ala	Val	Leu	Gln	Leu	Arg	Gly	Ala	Gly	Gly	Leu			
25		625				630					635					640			
	Pro	Ser	Ala	Ala	Ile	Gly	Gly	Gly	Val	Ala	Val	Gly	Glu	Pro	Val	Val			
					645					650					655				
	Ala	Met	Gly	Asn	Ser	Gly	Gly	Gln	Gly	Gly	Thr	Pro	Arg	Ala	Val	Pro			
30				660					665					670					
	Gly	Arg	Val	Val	Ala	Leu	Gly	Gln	Thr	Val	Gln	Ala	Ser	Asp	Ser	Leu			
			675					680					685						
35	Thr	Gly	Ala	Glu	Glu	Thr	Leu	Asn	Gly	Leu	Ile	Gln	Phe	Asp	Ala	Ala			
		690					695					700							
	Ile	Gln	Pro	Gly	Asp	Ala	Gly	Gly	Pro	Val	Val	Asn	Gly	Leu	Gly	Gln			
40		705				710					715					720			
	Val	Val	Gly	Met	Asn	Thr	Ala	Ala	Ser										
					725														
45	<210>	SEQ ID NO:19																	
	<211>	1797																	
	<212>	DNA																	
	<213>	Artificial Sequence																	
50	<223>	Description of Artificial Sequence:bi-fusion																	
		protein TbH9-Ra35 (designated Mtb59f)																	
	<222>	(1)..(1791)																	
	cat	atg	cat	cac	cat	cac	cat	cac	atg	gtg	gat	ttc	ggg	gcg	tta	cca			48
55	His	Met	His	His	His	His	His	His	Met	Val	Asp	Phe	Gly</						

	tcg	tgg	ata	ggt	tcg	tcg	gcg	ggg	ctg	atg	gtg	gcg	gcg	gcc	tcg	ccg	240
	Ser	Trp	Ile	Gly	Ser	Ser	Ala	Gly	Leu	Met	Val	Ala	Ala	Ala	Ser	Pro	
	65					70					75				80		
5	tat	gtg	gcg	tgg	atg	agc	gtc	acc	gcg	ggg	cag	gcc	gag	ctg	acc	gcc	288
	Tyr	Val	Ala	Trp	Met	Ser	Val	Thr	Ala	Gly	Gln	Ala	Glu	Leu	Thr	Ala	
					85					90					95		
10	gcc	cag	gtc	cgg	gtt	gct	gcg	gcg	gcc	tac	gag	acg	gcg	tat	ggg	ctg	336
	Ala	Gln	Val	Arg	Val	Ala	Ala	Ala	Ala	Tyr	Glu	Thr	Ala	Tyr	Gly	Leu	
				100					105					110			
15	acg	gtg	ccc	ccg	ccg	gtg	atc	gcc	gag	aac	cgt	gct	gaa	ctg	atg	att	384
	Thr	Val	Pro	Pro	Pro	Val	Ile	Ala	Glu	Asn	Arg	Ala	Glu	Leu	Met	Ile	
			115					120					125				
20	ctg	ata	gcg	acc	aac	ctc	ttg	ggg	caa	aac	acc	ccg	gcg	atc	gcg	gtc	432
	Leu	Ile	Ala	Thr	Asn	Leu	Leu	Gly	Gln	Asn	Thr	Pro	Ala	Ile	Ala	Val	
		130					135					140					
25	aac	gag	gcc	gaa	tac	ggc	gag	atg	tgg	gcc	caa	gac	gcc	gcc	gcg	atg	480
	Asn	Glu	Ala	Glu	Tyr	Gly	Glu	Met	Trp	Ala	Gln	Asp	Ala	Ala	Ala	Met	
	145					150					155					160	
30	ttt	ggc	tac	gcc	gcg	gcg	acg	gcg	acg	gcg	acg	gcg	acg	ttg	ctg	ccg	528
	Phe	Gly	Tyr	Ala	Ala	Ala	Thr	Ala	Thr	Ala	Thr	Ala	Thr	Leu	Leu	Pro	
				165					170					175			
35	ttc	gag	gag	gcg	ccg	gag	atg	acc	agc	gcg	ggg	ggg	ctc	ctc	gag	cag	576
	Phe	Glu	Glu	Ala	Pro	Glu	Met	Thr	Ser	Ala	Gly	Gly	Leu	Leu	Glu	Gln	
				180					185				190				
40	gcc	gcc	gcg	gtc	gag	gag	gcc	tcc	gac	acc	gcc	gcg	gcg	aac	cag	ttg	624
	Ala	Ala	Ala	Val	Glu	Glu	Ala	Ser	Asp	Thr	Ala	Ala	Ala	Asn	Gln	Leu	
			195					200				205					
45	atg	aac	aat	gtg	ccc	cag	gcg	ctg	caa	cag	ctg	gcc	cag	ccc	acg	cag	672
	Met	Asn	Asn	Val	Pro	Gln	Ala	Leu	Gln	Gln	Leu	Ala	Gln	Pro	Thr	Gln	
		210					215					220					
50	ggc	acc	acg	cct	tct	tcc	aag	ctg	ggg	ctg	tgg	aag	acg	gtc	tcg		720
	Gly	Thr	Thr	Pro	Ser	Ser	Lys	Leu	Gly	Gly	Leu	Trp	Lys	Thr	Val	Ser	
	225					230				235					240		
55	ccg	cat	cgg	tcg	ccg	atc	agc	aac	atg	gtg	tcg	atg	gcc	aac	aac	cac	768
	Pro	His	Arg	Ser	Pro	Ile	Ser	Asn	Met	Val	Ser	Met	Ala	Asn	Asn	His	
				245						250					255		
60	atg	tcg	atg	acc	aac	tcg	ggg	gtg	tcg	atg	acc	aac	acc				

	cag gca gtc acc ccg gcg gcg cgg gcg ctg ccg ctg acc agc ctg acc	1056
	Gln Ala Val Thr Pro Ala Ala Arg Ala Leu Pro Leu Thr Ser Leu Thr	
	340 345 350	
5	agc gcc gcg gaa aga ggg ccc ggg cag atg ctg ggc ggg ctg ccg gtg	1104
	Ser Ala Ala Glu Arg Gly Pro Gly Gln Met Leu Gly Gly Leu Pro Val	
	355 360 365	
10	ggg cag atg ggc gcc agg gcc ggt ggt ggg ctc agt ggt gtg ctg cgt	1152
	Gly Gln Met Gly Ala Arg Ala Gly Gly Gly Leu Ser Gly Val Leu Arg	
	370 375 380	
15	gtt ccg ccg cga ccc tat gtg atg ccg cat tct ccg gca gcc ggc gat	1200
	Val Pro Pro Arg Pro Tyr Val Met Pro His Ser Pro Ala Ala Gly Asp	
	385 390 395 400	
20	atc gcc ccg ccg gcc ttg tgc cag gac cgg ttc gcc gac ttc ccc gcg	1248
	Ile Ala Pro Pro Ala Leu Ser Gln Asp Arg Phe Ala Asp Phe Pro Ala	
	405 410 415	
25	ctg ccc ctc gac ccg tcc gcg atg gtc gcc caa gtg ggg cca cag gtg	1296
	Leu Pro Leu Asp Pro Ser Ala Met Val Ala Gln Val Gly Pro Gln Val	
	420 425 430	
30	gtc aac atc aac acc aaa ctg ggc tac aac aac gcc gtg ggc gcc ggg	1344
	Val Asn Ile Asn Thr Lys Leu Gly Tyr Asn Asn Ala Val Gly Ala Gly	
	435 440 445	
35	acc ggc atc gtc atc gat ccc aac ggt gtc gtg ctg acc aac aac cac	1392
	Thr Gly Ile Val Ile Asp Pro Asn Gly Val Val Leu Thr Asn Asn His	
	450 455 460	
40	gtg atc gcg ggc gcc acc gac atc aat gcg ttc agc gtc ggc tcc ggc	1440
	Val Ile Ala Gly Ala Thr Asp Ile Asn Ala Phe Ser Val Gly Ser Gly	
	465 470 475 480	
45	caa acc tac ggc gtc gat gtg gtc ggg tat gac cgc acc cag gat gtc	1488
	Gln Thr Tyr Gly Val Asp Val Val Gly Tyr Asp Arg Thr Gln Asp Val	
	485 490 495	
50	gcg gtg ctg cag ctg cgc ggt gcc ggt ggc ctg ccg tgc gcg gcg atc	1536
	Ala Val Leu Gln Leu Arg Gly Ala Gly Gly Leu Pro Ser Ala Ala Ile	
	500 505 510	
55	ggt ggc ggc gtc gcg gtt ggt gag ccc gtc gtc gcg atg ggc aac agc	1584
	Gly Gly Gly Val Ala Val Gly Glu Pro Val Val Ala Met Gly Asn Ser	
	515 520 525	
60	ggt ggg cag ggc gga acg ccc cgt gcg gtg cct ggc agg gtg gtc gcg	1632
	Gly Gly Gln Gly Gly Thr Pro Arg Ala Val Pro Gly Arg Val Val Ala	
	530 535 540	
65	ctc ggc caa acc gtg cag gcg tgc gat tgc ctg acc ggt gcc gaa gag	1680
	Leu Gly Gln Thr Val Gln Ala Ser Asp Ser Leu Thr Gly Ala Glu Glu	
	545 550 555 560	
70	aca ttg aac ggg ttg atc cag ttc gat gcc gcg atc cag ccc ggt gat	1728
	Thr Leu Asn Gly Leu Ile Gln Phe Asp Ala Ala Ile Gln Pro Gly Asp	
	565 570 575	
75	tgc ggc ggg ccc gtc gtc aac ggc cta gga cag gtg gtc ggt atg aac	1776
	Ser Gly Gly Pro Val Val Asn Gly Leu Gly Gln Val Val Gly Met Asn	
	580 585 590	
80	acg gcc gcg tcc taggatatc	1797
	Thr Ala Ala Ser	
	595	

<210> SEQ ID NO:20

<211> 596

<212> PRT

5 <213> Artificial Sequence

<223> Description of Artificial Sequence:bi-fusion
protein TbH9-Ra35 (designated Mtb59f)

10 His Met His His His His His Met Val Asp Phe Gly Ala Leu Pro
1 5 10 15
Pro Glu Ile Asn Ser Ala Arg Met Tyr Ala Gly Pro Gly Ser Ala Ser
20 25 30
15 Leu Val Ala Ala Ala Gln Met Trp Asp Ser Val Ala Ser Asp Leu Phe
35 40 45
Ser Ala Ala Ser Ala Phe Gln Ser Val Val Trp Gly Leu Thr Val Gly
50 55 60
20 Ser Trp Ile Gly Ser Ser Ala Gly Leu Met Val Ala Ala Ala Ser Pro
65 70 75 80
25 Tyr Val Ala Trp Met Ser Val Thr Ala Gly Gln Ala Glu Leu Thr Ala
85 90 95
Ala Gln Val Arg Val Ala Ala Ala Ala Tyr Glu Thr Ala Tyr Gly Leu
100 105 110
30 Thr Val Pro Pro Pro Val Ile Ala Glu Asn Arg Ala Glu Leu Met Ile
115 120 125
Leu Ile Ala Thr Asn Leu Leu Gly Gln Asn Thr Pro Ala Ile Ala Val
130 135 140
35 Asn Glu Ala Glu Tyr Gly Glu Met Trp Ala Gln Asp Ala Ala Ala Met
145 150 155 160
40 Phe Gly Tyr Ala Ala Ala Thr Ala Thr Ala Thr Ala Thr Leu Leu Pro
165 170 175
Phe Glu Glu Ala Pro Glu Met Thr Ser Ala Gly Gly Leu Leu Glu Gln
180 185 190
45 Ala Ala Ala Val Glu Glu Ala Ser Asp Thr Ala Ala Ala Asn Gln Leu
195 200 205
Met Asn Asn Val Pro Gln Ala Leu Gln Gln Leu Ala Gln Pro Thr Gln
210 215 220
50 Gly Thr Thr Pro Ser Ser Lys Leu Gly Gly Leu Trp Lys Thr Val Ser
225 230 235 240
Pro His Arg Ser Pro Ile Ser Asn Met Val Ser Met Ala Asn Asn His
245 250 255
55 Met Ser Met Thr Asn Ser Gly Val Ser Met Thr Asn Thr Leu Ser Ser
260 265 270
60 Met Leu Lys Gly Phe Ala Pro Ala Ala Ala Ala Gln Ala Val Gln Thr
275 280 285
Ala Ala Gln Asn Gly Val Arg Ala Met Ser Ser Leu Gly Ser Ser Leu
290 295 300
65 Gly Ser Ser Gly Leu Gly Gly Gly Val Ala Ala Asn Leu Gly Arg Ala
305 310 315 320
Ala Ser Val Gly Ser Leu Ser Val Pro Gln Ala Trp Ala Ala Ala Asn


```

ACAGTACATC GGCCTTGTCTG AGTCGGTTGC CGGCTCCTGC AACAACTATT AAGCCCATGC      300
GGGCCCCATC CCGCGACCCG GCATCGTCGC CGGGGCTAGG CCAGATTGCC CCGCTCCTCA      360
ACGGGCGGCA TCCCGCGACC CGGCATCGTC GCCGGGGCTA GGCCAGATTG CCCCCTCCT      420
CAACGGGGCCG CATCTCGTGC CGAATTCCTG CAGCCCGGGG GATCCACTAG TTCTAGAGCG      480
5 GCCGCCACCG CCGTGGAGCT                                     500

```

(2) INFORMATION FOR SEQ ID NO:22: DPV (MTB8.4)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 96 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

```

Val Ala Met Ser Leu Thr Val Gly Ala Gly Val Ala Ser Ala Asp Pro
1          5          10          15
Val Asp Ala Val Ile Asn Thr Thr Cys Asn Tyr Gly Gln Val Val Ala
20          20          25          30
Ala Leu Asn Ala Thr Asp Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser
35          40          45
Pro Val Ala Gln Ser Tyr Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro
25          50          55          60
Gln Arg Ala Ala Met Ala Ala Gln Leu Gln Ala Val Pro Gly Ala Ala
65          70          75          80
Gln Tyr Ile Gly Leu Val Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr
85          90          95

```

(2) INFORMATION FOR SEQ ID NO:23: MSL (MTB9.8)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 585 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

```

TGGATTCCGA TAGCGTTTTC GGCCCTCGA CGGGCGACCA CGGCGCGCAG GCCTCCGAAC      60
GGGGGGCCGG GACGCTGGGA TTCGCCGGA CCGCAACCAA AGAACGCCGG GTCCGGGCGG      120
TCGGGCTGAC CGCACTGGCC GGTGATGAGT TCGGCAACGG CCCCCTGATG CCGATGGTGC      180
CGGGGACCTG GGAGCAGGGC AGCAACGAGC CCGAGGCGCC CGACGGATCG GGGAGAGGGG      240
GAGGCGACGG CTTACCGCAC GACAGCAAGT AACCAGATTC CGAATCACGT GGACCCGTAC      300
GGGTCGAAAG GAGAGATGTT ATGAGCCTTT TGGATGCTCA TATCCACAG TTGGTGGCCT      360
CCCAGTCGGC GTTTGCCGCC AAGGCGGGGC TGATGCGGCA CACGATCGGT CAGGCCGAGC      420
AGGCGGCGAT GTCGGCTCAG GCGTTTCACC AGGGGGAGTC GTCGGCGGCG TTTCAGGCCG      480
55 CCCATGCCCG GTTGTGGCG GCGGCCGCCA AAGTCAACAC CTTGTTGGAT GTCGCGCAGG      540
CGAATCTGGG TGAGGCCGCC GGTACCTATG TGGCCGCCGA TGCTG                                     585

```

(2) INFORMATION FOR SEQ ID NO:24: MSL (MTB9.8)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 97 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:24:

```

Met Ser Leu Leu Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser
 1      5      10      15
5  Ala Phe Ala Ala Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala
    20      25      30
    Glu Gln Ala Ala Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser
    35      40      45
10  Ala Ala Phe Gln Ala Ala His Ala Arg Phe Val Ala Ala Ala Ala Lys
    50      55      60
    Val Asn Thr Leu Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala
    65      70      75      80
    Gly Thr Tyr Val Ala Ala Asp Ala Ala Ala Ser Thr Tyr Thr Gly
    85      90      95
15  Phe

```

(2) INFORMATION FOR SEQ ID NO:25: MTI (MTB9.9A)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1742 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: double
 (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
 (A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:25:

```

CCGCTCTCTT TCAACGTCAT AAGTTCGGTG GGCCAGTCGG CCGCGCGTGC ATATGGCACC      60
AATAACGCGT GTCCCATGGA TACCCGGACC GCACGACGGT AGAGCGGATC AGCGCAGCCG      120
35  GTGCGGAACA CTACCGCGTC CACGCTCAGC CCTGCCGCGT TGCAGGAAGT CGAGCCCAGG      180
    TTCTCATGGT CGTTAACGCC TTCCAACACT GCGACGGTGC GCGCCCCGGC GACCACCTGA      240
    GCAAACGCTCG GCTCCGGCAC CCGGCGCGCG GCTGCCAACA CCCCACGATT GAGATGGAAG      300
    CCGATCACCC GTGCCATGAC ATCAGCCGAC GCTCGATAGT ACGGCGCGCC GACACCGGCC      360
    AGATCATCCT TGAGCTCGGC CAGCCGGCGG TCGGTGCCGA ACAGCGCCAG CGGCGTGAAC      420
40  CGTGAGGCCA GCATGCGCTG CACCACCAGC ACACCTCTCG CGATCACCAA CGCCTTGCCG      480
    GTCGGCAGAT CGGGACNACN TTCGATGCTG TTCAGGTCAC GGAAATCGTC GAGCCGTGGG      540
    TCGTCGGGAT CGCAGACGTC CTGAACATCG AGGCCGTCGG GGTGCTGGGC ACAACGGCCT      600
    TCGGTACCGG GCTTTCGTCG ACCAGAGCCA GCATCAGATC GGCGGCGCTG CGCAGGATGT      660
    CACGCTCGCT GCGGTTTCAG GTCGCGAGCC GCTCAGCCAG CCACTCTTGC AGAGAGCCGT      720
45  TGCTGGGATT AATTGGGAGA GGAAGACAGC ATGTCTGTCG TGACCACACA GCCGGAAGCC      780
    CTGGCAGCTG CGGCGGCGAA CCTACAGGGT ATTGGCACGA CAATGAACGC CCAGAACGCG      840
    GCCGCGGCTG CTCCAACCAC CGGAGTAGTG CCGCAGCCG CCGATGAAGT ATCAGCGCTG      900
    ACCGCGGCTC AGTTTGCTGC GCACGCGCAG ATGTACCAA CGGTACGCGC CCAGGCCGCG      960
50  GCCATTACAG AATGTTTCGT GAACACGCTG GTGGCCAGTT CTGGCTCATA CGCGGCCACC      1020
    GAGGCGGCCA ACGCAGCCGC TGCCGGCTGA ACGGGCTCGC ACGAACCTGC TGAAGGAGAG      1080
    GGGGAACATC CGGAGTTCTC GGGTCAGGGG TTGCGCCAGC GCCCAGCCGA TTCAGNTATC      1140
    GCGTCCATA ACAGCAGACG ATCTAGGCAT TCAGTACTAA GGAGACAGGC AACATGGCCT      1200
    CACGTTTTAT GACGGATCCG CATGCGATGC GGGACATGGC GGGCCGTTTT GAGGTGCACG      1260
    CCCAGACGGT GGAGACGAG GCTCGCCGGA TGTGGGCGTC CGCGCAAAAC ATTTCCGGTG      1320
55  CGGGCTGGAG TGGCATGGCC GAGGCGACCT CGCTAGACAC CATGACCTAG ATGAATCAGG      1380
    CGTTTCGCAA CATCGTGAAC ATGCTGCACG GGGTGCGTGA CGGGCTGGTT CGCGACGCCA      1440
    ACAANTACGA ACAGCAAGAG CAGGCCTCCC AGCAGATCCT GAGCAGNTAG CGCCGAAAGC      1500
    CACAGCTGNG TACGNTTCT CACATTAGGA GAACACCAAT ATGACGATTA ATTACAGTT      1560
    CGGGGACGTC GACGCTCATG GCGCCATGAT CCGCGCTCAG GCGGCGTCGC TTGAGGCGGA      1620
60  GCATCAGGCC ATCGTTCGTG ATGTGTTGGC CGCGGGTGAC TTTTGGGGCG GCGCCGGTTC      1680
    GGTGGCTTGC CAGGAGTTCA TTACCCAGTT GGGCCGTAAC TTCCAGGTGA TCTACGAGCA      1740
    GG

```

(2) INFORMATION FOR SEQ ID NO:26: MTI (MTB9.9A)

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 2836 base pairs

(B) TYPE: nucleic acid
(C) STRANDEDNESS: double
(D) TOPOLOGY: linear

5 (ii) MOLECULE TYPE: DNA (genomic)

(vi) ORIGINAL SOURCE:
(A) ORGANISM: Mycobacterium tuberculosis

10 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:26:

	GTTGATTCCG	TTCGCGGCGC	CGCCGAAGAC	CACCAACTCC	GCTGGGGTGG	TCGCACAGGC	60
	GGTTGCGTCG	GTCAGCTGGC	CGAATCCCAA	TGATTGGTGG	CTCNGTGC GG	TTGCTGGGCT	120
	CGATTACCCC	CACGGAAAGG	ACGACGATCG	TTCTGTTGCT	CGGTCAGTCG	TACTTGGCGA	180
15	CGGGCATGGC	GCGGTTTCTT	ACCTCGATCG	CACAGCAGCT	GACCTTCGGC	CCAGGGGGCA	240
	CAACGGCTGG	CTCCGGCGGA	GCCTGGTACC	CAACGCCACA	ATTGCGCCGC	CTGGGTGCAG	300
	GCCCGGCGGT	GTCGGCGAGT	TTGGCGCGGG	CGGAGCCGGT	CGGGAGGTTG	TCGGTGCCGC	360
	CAAGTTGGGC	CGTCGCGGCT	CCGGCCTTCG	CGGAGAAGCC	TGAGGCGGGC	ACGCCGATGT	420
	CCGTCATCGG	CGAAGCGTCC	AGCTGCGGTC	AGGGAGGCCT	GCTTCGAGGC	ATACCGCTGG	480
20	CGAGAGCGGG	GCGGCGTACA	GGCGCCTTCG	CTCACCATA	CGGGTTCGCG	CACAGCGTGA	540
	TTACCCGGTC	TCCGTCGGCG	GGATAGCTTT	CGATCCGGTC	TGCGCGGCCG	CCGGAATGCG	600
	TGCAGATAGC	GATCGACCGC	GCCGGTCGGT	AAACGCCGCA	CACGGCACTA	TCAATGCGCA	660
	CGGCGGGCGT	TGATGCCAAA	TTGACCGTCC	CGACGGGGCT	TTATCTGCGG	CAAGATTTCA	720
	TCCCCAGCCC	GGTCGGTGGG	CCGATAAATA	CGCTGCTCAG	CGCGACTCTT	CCGGCTGAAT	780
25	TCGATGCTCT	GGGCGCCCGC	TCGACGCCGA	GTATCTCGAG	TGGGCCGCAA	ACCCGGTCAA	840
	ACGCTGTTAC	TGTGGCGTTA	CCACAGGTGA	ATTTGCGGTG	CCAAGTGGTG	AACACTTGCG	900
	AACGGGTGGC	ATCGAAATCA	ACTTGTTCGG	TTGCAGTGAT	CTACTCTCTT	GCAGAGAGCC	960
	GTTGCTGGGA	TTAATTGGGA	GAGGAAGACA	GCATGTCGTT	CGTGACCACA	CAGCCGGAAG	1020
	CCCTGGCAGC	TGCGGCGGCG	AACCTACAGG	GTATTGGCAC	GACAATGAAC	GCCCAGAACG	1080
30	CGGCCGCGGC	TGCTCCAACC	ACCGGAGTAG	TGCCCGCAGC	CGCCGATGAA	GTATCAGCGC	1140
	TGACCGCGGC	TCAGTTTGCT	GCGCACGCGC	AGATGTACCA	AACGGTCAGC	GCCCAGGCCG	1200
	CGGCCATTCA	CGAAATGTTT	GTGAACACGC	TGGTGGCCAG	TTCTGGCTCA	TACGCGGCCA	1260
	CCGAGGCGGC	CAACGCAGCC	GCTGCCGGCT	GAACGGGCTC	GCACGAACCT	GCTGAAGGAG	1320
	AGGGGGAACA	TCCGGAGTTC	TCCGGGTCAGG	GGTTGCGCCA	GCGCCAGCC	GATTCAGCTA	1380
35	TCGGCGTCCA	TAACAGCAGA	CGATCTAGGC	ATTCTAGTACT	AAGGAGACAG	GCAACATGGC	1440
	CTCACGTTTT	ATGACGGATC	CGCATGCGAT	GCGGGACATG	GCGGGCCGTT	TTGAGGTGCA	1500
	CGCCAGACAG	GTGGAGGACG	AGGCTCGCCG	GATGTGGGCG	TCCGCGCAAA	ACATTTCCGG	1560
	TGCGGGCTGG	AGTGGCATGG	CCGAGGCGAC	CTCGCTAGAC	ACCATGACCT	AGATGAATCA	1620
	GGCGTTTCGC	AACATCGTGA	ACATGCTGCA	CGGGGTGCGT	GACGGGCTGG	TTCCGCGACG	1680
40	CAACAACTAC	GAACAGCAAG	AGCAGGCCTC	CCAGCAGATC	CTGAGCAGCT	AGCGCCGAAA	1740
	GCCACAGCTG	CGTACGCTTT	CTCACATTAG	GAGAACACCA	ATATGACGAT	TAATTACCAG	1800
	TTTCGGGACG	TCGACGCTCA	TGGCGCCATG	ATCCGCGCTC	AGGCGCGGTC	GCTTGAGGCG	1860
	GAGCATCAGG	CCATCGTTTC	TGATGTGTTG	GCCGCGGGTG	ACTTTTGGGG	CGGCGCCGGT	1920
	TCGGTGGCTT	GCCAGGAGTT	CATTACCCAG	TTGGGCCGTA	ACTTCCAGGT	GATCTACGAG	1980
45	CAGGCCAACG	CCCACGGGCA	GAAGGTGCAG	GCTGCCGGCA	ACAACATGGC	GCAAACCGAC	2040
	AGCGCCGTCG	GCTCCAGCTG	GGCCTAAAAC	TGAACCTCAG	TCGCGGCAGC	ACACCAACCA	2100
	GCCGGTGTGC	TGCTGTGTCC	TGCAGTTAAT	TAGCACTCGA	CCGCTGAGGT	AGCGATGGAT	2160
	CAACAGAGTA	CCCCCACCAG	CATCACCGTC	AACGTCGACG	GCTTCTGGAT	GCTTCAGGCG	2220
	CTACTGGATA	TCCGCCACGT	TGCGCCTGAG	TTACGTTGCC	GGCCGTACGT	CTCCACCGAT	2280
50	TCCAATGACT	GGCTAAACGA	GCACCCGGGG	ATGGCGGTCA	TGCGCGAGCA	GGGCATTGTC	2340
	GTCAACGACG	CGGTCAACGA	ACAGGTCGCT	GCCCGGATGA	AGGTGCTTGC	CGCACCTGAT	2400
	CTTGAAGTCG	TCCGCCCTGCT	GTCACGCGGC	AAGTTGCTGT	ACGGGGTCAT	AGACGACGAG	2460
	AACCAGCCGC	CGGGTTTCGCG	TGACATCCCT	GACAATGAGT	TCCGGGTGGT	GTTGGCCCCG	2520
	CGAGGCCAGC	ACTGGGTGTC	GGCGGTACGG	GTTGGCAATG	ACATCACCGT	CGATGACGTG	2580
55	ACGGTCTCGG	ATAGCGCCTC	GATCGCCGCA	CTGGTAATGG	ACGGTCTGGA	GTGATTTCAC	2640
	CACGCCGACC	CAGCCGCGAT	CAACGCGGTC	AACGTGCCAA	TGGAGGAGAT	CTCGTGCCGA	2700
	ATTTCGGCACG	AGGCACGAGG	CGGTGTCCGT	GACGACGGGA	TCGATCACGA	TCATCGACCG	2760
	GCCGGGATCC	TTGGCGATCT	CGTTGAGCAC	GACCCGGGCC	CGCGGGAAGC	TCTGCGACAT	2820
60	CCATGGGTTC	TTCCCG					2836

(2) INFORMATION FOR SEQ ID NO:27: MTI (MTB9.9A)

65 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 94 amino acids
(B) TYPE: amino acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: peptide

(vi) ORIGINAL SOURCE:

(A) ORGANISM: Mycobacterium tuberculosis

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:27:

Met Thr Ile Asn Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met
1 5 10 15
Ile Arg Ala Leu Ala Gly Leu Leu Glu Ala Glu His Gln Ala Ile Ile
20 25 30
Ser Asp Val Leu Thr Ala Ser Asp Phe Trp Gly Gly Ala Gly Ser Ala
35 40 45
Ala Cys Gln Gly Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile
50 55 60
Tyr Glu Gln Ala Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn
65 70 75 80
Asn Met Ala Gln Thr Asp Ser Ala Val Gly Ser Ser Trp Ala
85 90

(2) INFORMATION FOR SEQ ID NO:28: HTCC#1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 1200 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: cDNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

CAGGCATGAG CAGAGCGTTC ATCATCGATC CAACGATCAG TGCCATTGAC GGCTTGTACG 60
ACCTTCTGGG GATTGGAATA CCCAACCAGG GGGGTATCCT TTACTCCTCA CTAGAGTACT 120
TCGAAAAAGC CCTGGAGGAG CTGGCAGCAG CGTTTCCGGG TGATGGCTGG TTAGGTTCCG 180
CCGCGGACAA ATACGCCGGC AAAAACCAGC ACCACGTGAA TTTTTCAG GAACTGGCAG 240
ACCTCGATCG TCAGCTCATC AGCCTGATCC ACGACCAGGC CAACGCGGTC CAGACGACCC 300
GCGACATCCT GGAGGGCGCC AAGAAAGGTC TCGAGTTCGT GCGCCCGGTG GCTGTGGACC 360
TGACCTACAT CCCGGTCGTC GGGCACGCCC TATCGGCCGC CTTCCAGGCG CCGTTTTGCG 420
CGGGCGCGAT GGCCGTAGTG GGC GGCGCGCGC TTGCCTACTT GGTCGTGAAA ACGCTGATCA 480
ACGCGACTCA ACTCCTCAAA TTGCTTGCCA AATTGGCGGA GTTGGTCGCG GCCGCCATTG 540
CGGACATCAT TTCGGATGTG GCGGACATCA TCAAGGGCAC CCTCGGAGAA GTGTGGGAGT 600
TCATCACAAA CGCGCTCAAC GGCCTGAAAG AGCTTTGGGA CAAGCTCACG GGGTGGGTGA 660
CCGGAAGTGT CTCTCGAGGG TGGTCGAACC TGAGATCCTT CTTTGGCGGC GTCCCCGGCT 720
TGACCGGCGC GACCAGCGGC TTGTGCGAAG TGAAGTGGCT GTTCGGTGCG GCCGGTCTGT 780
CCGCATCGTC GGGCTTGGCT CACGCGGATA GCCTGGCGAG CTCAGCCAGC TTGCCCCGCC 840
TGGCCGGCAT TGGGGGCGGG TCCGGTTTGT GGGGCTTGCC GAGCCTGGCT CAGGTCCATG 900
CCGCCTCAAC TCGGCAGGCG CTACGGCCCC GAGCTGATGG CCCGGTCGGC GCCGCTGCCG 960
AGCAGGTCGG CGGGCAGTCG CAGCTGGTCT CCGCGCAGGG TTCCCAAGGT ATGGGCGGAC 1020
CCGTAGGCAT GGGCGGCATG CACCCCTCTT CGGGGCGGTC GAAAGGGACG ACGACGAAGA 1080
AGTACTCGGA AGGCGCGGCG GCGGGCACTG AAGACGCCGA GCGCGCGCCA GTCGAAGCTG 1140
ACGCGGGCGG TGGGCAAAAG GTGCTGTGAC GAAACGTCGT CTAACGGCAT GGCGAGCCAA 1200

(2) INFORMATION FOR SEQ ID NO:29: HTCC#1

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 392 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

5	Met 1	Ser	Arg	Ala	Phe 5	Ile	Ile	Asp	Pro	Thr 10	Ile	Ser	Ala	Ile	Asp 15	Gly
	Leu	Tyr	Asp	Leu	Leu	Gly	Ile	Gly	Ile	Pro	Asn	Gln	Gly	Gly	Ile	Leu
	Tyr	Ser	Ser	20	Glu	Tyr	Phe	Glu	Lys	Ala	Leu	Glu	Glu	Leu	Ala	Ala
				35			40				45					
10	Ala	Phe	Pro	Gly	Asp	Gly	Trp	Leu	Gly	Ser	Ala	Ala	Asp	Lys	Tyr	Ala
	50						55				60					
	Gly	Lys	Asn	Arg	Asn	His	Val	Asn	Phe	Phe	Gln	Glu	Leu	Ala	Asp	Leu
	65				70						75					80
15	Asp	Arg	Gln	Leu	Ile	Ser	Leu	Ile	His	Asp	Gln	Ala	Asn	Ala	Val	Gln
					85					90					95	
	Thr	Thr	Arg	Asp	Ile	Leu	Glu	Gly	Ala	Lys	Lys	Gly	Leu	Glu	Phe	Val
				100					105					110		
20	Arg	Pro	Val	Ala	Val	Asp	Leu	Thr	Tyr	Ile	Pro	Val	Val	Gly	His	Ala
				115					120					125		
	Leu	Ser	Ala	Ala	Phe	Gln	Ala	Pro	Phe	Cys	Ala	Gly	Ala	Met	Ala	Val
							135					140				
25	Val	Gly	Gly	Ala	Leu	Ala	Tyr	Leu	Val	Val	Lys	Thr	Leu	Ile	Asn	Ala
	145				150						155					160
	Thr	Gln	Leu	Leu	Lys	Leu	Leu	Ala	Lys	Leu	Ala	Glu	Leu	Val	Ala	Ala
					165					170					175	
30	Ala	Ile	Ala	Asp	Ile	Ile	Ser	Asp	Val	Ala	Asp	Ile	Ile	Lys	Gly	Thr
				180					185					190		
	Leu	Gly	Glu	Val	Trp	Glu	Phe	Ile	Thr	Asn	Ala	Leu	Asn	Gly	Leu	Lys
				195				200					205			
35	Glu	Leu	Trp	Asp	Lys	Leu	Thr	Gly	Trp	Val	Thr	Gly	Leu	Phe	Ser	Arg
							215				220					
	Gly	Trp	Ser	Asn	Leu	Glu	Ser	Phe	Phe	Ala	Gly	Val	Pro	Gly	Leu	Thr
	225				230						235				240	
40	Gly	Ala	Thr	Ser	Gly	Leu	Ser	Gln	Val	Thr	Gly	Leu	Phe	Gly	Ala	Ala
					245					250					255	
	Gly	Leu	Ser	Ala	Ser	Ser	Gly	Leu	Ala	His	Ala	Asp	Ser	Leu	Ala	Ser
				260					265					270		
45	Ser	Ala	Ser	Leu	Pro	Ala	Leu	Ala	Gly	Ile	Gly	Gly	Gly	Ser	Gly	Phe
				275					280					285		
	Gly	Gly	Leu	Pro	Ser	Leu	Ala	Gln	Val	His	Ala	Ala	Ser	Thr	Arg	Gln
				290				295				300				
50	Ala	Leu	Arg	Pro	Arg	Ala	Asp	Gly	Pro	Val	Gly	Ala	Ala	Ala	Glu	Gln
	305				310						315					320
	Val	Gly	Gly	Gln	Ser	Gln	Leu	Val	Ser	Ala	Gln	Gly	Ser	Gln	Gly	Met
					325					330					335	
55	Gly	Gly	Pro	Val	Gly	Met	Gly	Gly	Met	His	Pro	Ser	Ser	Gly	Ala	Ser
				340					345					350		
	Lys	Gly	Thr	Thr	Lys	Lys	Tyr	Ser	Glu							

55 (i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 1441 base pairs
(B) TYPE: nucleic acid
(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

100


```

CGGCACGAGA GACCGATGCC GCTACCCTCG CGCAGGAGGC AGGTAATTTTC GAGCGGATCT      60
CCGCGCGACCT GAAAACCCAG ATCGACCAGG TGGAGTCGAC GGCAGGTTTC TTGCAGGGCC      120
AGTGGCGCGG CGCGGCGGGG ACGGCCGCCC AGGCCGCGGT GGTGCGCTTC CAAGAAGCAG      180
CCAATAAGCA GAAGCAGGAA CTCGACGAGA TCTCGACGAA TATTCGTCAG GCCGCGGTCC      240
5 AATACTCGAG GGCCGACGAG GAGCAGCAGC AGGCGCTGTC CTCGCAAATG GGCTTCTGAC      300
CCGCTAATAC GAAAAGAAAC GGAGCAA      327

```

(2) INFORMATION FOR SEQ ID NO:35: Tb38-1

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 95 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

```

Thr Asp Ala Ala Thr Leu Ala Gln Glu Ala Gly Asn Phe Glu Arg Ile
1      5      10      15
Ser Gly Asp Leu Lys Thr Gln Ile Asp Gln Val Glu Ser Thr Ala Gly
20      25      30
Ser Leu Gln Gly Gln Trp Arg Gly Ala Ala Gly Thr Ala Ala Gln Ala
35      40      45
Ala Val Val Arg Phe Gln Glu Ala Ala Asn Lys Gln Lys Gln Glu Leu
50      55      60
Asp Glu Ile Ser Thr Asn Ile Arg Gln Ala Gly Val Gln Tyr Ser Arg
65      70      75      80
Ala Asp Glu Glu Gln Gln Gln Ala Leu Ser Ser Gln Met Gly Phe
85      90      95

```

(2) INFORMATION FOR SEQ ID NO:36: TbRa3

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 542 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

```

GAATTCGGCA CGAGAGGTGA TCGACATCAT CGGGACCAGC CCCACATCCT GGGAACAGGC      60
GGCGGCGGAG GCGGTCCAGC GGGCGCGGGA TAGCGTCGAT GACATCCGCG TCGCTCGGGT      120
45 CATTGAGCAG GACATGGCCG TGGACAGCGC CGGCAAGATC ACCTACCGCA TCAAGCTCGA      180
AGTGTCGTTT AAGATGAGGC CGGCGCAACC GCGCTAGCAC GGGCCGGCGA GCAAGACGCA      240
AAATCGCACG GTTTGCGGTT GATTCGTGCG ATTTTGTGTC TGCTCGCCGA GGCCTACCAG      300
GCGCGGCCCA GGTCCGCGTG CTGCCGTATC CAGGCGTGCA TCGCGATTCC GGCGGCCACG      360
CCGGAGTTAA TGCTTCGCGT CGACCCGAAC TGGGCGATCC GCCGNGAGC TGATCGATGA      420
50 CCGTGCCAG CCCGTCGATG CCCGAGTTGC CCGAGGAAAC GTGCTGCCAG GCCGGTAGGA      480
AGCGTCCGTA GGCGGCGGTG CTGACCGGCT CTGCCTGCGC CCTCAGTGCG GCCAGCGAGC      540
GG      542

```

(2) INFORMATION FOR SEQ ID NO:37: TbRa3

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 66 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

```

Val Ile Asp Ile Ile Gly Thr Ser Pro Thr Ser Trp Glu Gln Ala Ala
1      5      10      15
Ala Glu Ala Val Gln Arg Ala Arg Asp Ser Val Asp Asp Ile Arg Val
20      25      30

```

Ala Arg Val Ile Glu Gln Asp Met Ala Val Asp Ser Ala Gly Lys Ile
 35 40 45
 Thr Tyr Arg Ile Lys Leu Glu Val Ser Phe Lys Met Arg Pro Ala Gln
 50 55 60
 Pro Arg
 65

(2) INFORMATION FOR SEQ ID NO:38: 38 kD

- (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 1993 base pairs
 (B) TYPE: nucleic acid
 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

TGTTCTTCGA CGGCAGGCTG GTGGAGGAAG GGCCCACCGA ACAGCTGTTC TCCTCGCCGA 60
 AGCATGCGGA AACCGCCCGA TACGTCGCCG GACTGTCTGGG GGACGTCAAG GACGCCAAGC 120
 GCGGAAATTG AAGAGCACAG AAAGGTATGG CGTGAAATT CGTTGCATA CGCTGTTGGC 180
 CGTGTTGACC GCTGCGCCGC TGCTGCTAGC AGCGGCGGGC TGTGGCTCGA AACCACCGAG 240
 CGTTTCGCCT GAAACGGGCG CCGGCGCCCG TACTGTCTGG ACTACCCCG CGTCGTCTGC 300
 GGTGACGTTG GCGGAGACCG GTAGCACGCT GCTCTACCCG CTGTTCAACC TGTGGGGTCC 360
 GGCCTTTTAC GAGAGGTATC CGAACGTCAC GATCACCGCT CAGGGCACCG GTTCTGGTGC 420
 CGGGATCGCG CAGGCCGCGC CCGGGACGGT CAACATTGGG GCCTCCGACG CCTATCTGTC 480
 GGAAGGTGAT ATGGCCGCGC ACAAGGGGCT GATGAACATC GCGCTAGCCA TCTCCGCTCA 540
 GCAGGTCAAC TACAACCTGC CCGGAGTGAG CGAGCACCTC AAGTGAAACG GAAAAGTCCT 600
 GCGCGCCATG TACCAGGGCA CCATCAAAAC CTGGGACGAC CCGCAGATCG CTGCGCTCAA 660
 CCCC GGCGTG AACCTGCCCC GCACCGCGGT AGTTCCGCTG CACCGCTCCG ACGGGTCCGG 720
 TGACACCTTC TTGTTACCC AGTACCTGTC CAAGCAAGAT CCCGAGGGCT GGGGCAAGTC 780
 GCGCGGCTTC GGCACCACCG TCGACTTCCC GCGGGTGCCG GGTGCGCTGG GTGAGAACGG 840
 CAACGGCGGC ATGGTGACCG GTTGCGCCGA GACACCGGGC TGCCTGGCCT ATATCGGCAT 900
 CAGCTTCCTC GACCAGGCCA GTCAACGGGG ACTCGGCGAG GCCCACTAG GCAATAGCTC 960
 TGGCAATTC TTGTTGCCCG ACGCGCAAAG CATTCAAGCC GCGGCGGCTG GCTTCGCATC 1020
 GAAAACCCCG GCGAACCAGG CGATTTTCAT GATCGACGGG CCCGCCCCCG ACGGCTACCC 1080
 GATCATCAAC TACGAGTACG CCATCGTCAA CAACCGGCAA AAGGACGCCG CCACCGCGCA 1140
 GACCTTGACG GCATTTCTGC ACTGGGCGAT CACCGACGGC AACAAGGCCT CGTTCCTCGA 1200
 CCAGGTTTCAT TTCCAGCCGC TGCCGCCCGC GGTGGTGAAG TTGTCTGACG CGTTGATCGC 1260
 GACGATTTCC AGCTAGCCTC GTTGACCACC ACGCGACAGC AACCTCCGTC GGGCCATCGG 1320
 GCTGCTTTGC GGAGCATGCT GGGCCGTGCC GGTGAAGTCG GCCGCGCTGG CCCGGCCATC 1380
 CGGTGGTTGG GTGGGATAGG TGCGGTGATC CCGCTGCTTG CGCTGGTCTT GGTGCTGGTG 1440
 GTGCTGGTCA TCGAGGCGAT GGGTGCGATC AGGCTCAACG GGTTGCATTT CTTACCGCC 1500

```

ACCGAATGGA ATCCAGGCAA CACCTACGGC GAAACCGTTG TCACCGACGC GTCGCCCATC 1560
CGGTGCGGCG CTACTACGGG GCGTTGCCGC TGATCGTCGG GACGCTGGCG ACCTCGGCAA 1620
5 TCGCCCTGAT CATCGCGGTG CCGGTCTCTG TAGGAGCGGC GCTGGTGATC GTGGAACGGC 1680
TGCCGAAACG GTTGGCCGAG GCTGTGGGAA TAGTCTGGA ATTGCTCGCC GGAATCCCCA 1740
10 GCGTGGTCGT CGGTTTGTGG GGGGCAATGA CGTTCGGGCC GTTCATCGCT CATCACATCG 1800
CTCCGGTGAT CGCTCACAAC GCTCCCGATG TGCCGGTGCT GAACTACTTG CGCGGCGACC 1860
CGGGCAACGG GGAGGGCATG TTGGTGTCCG GTCTGGTGTT GCGGGTGATG GTCGTTCCCA 1920
15 TTATCGCCAC CACCACTCAT GACCTGTTCG GGCAGGTGCC GGTGTTGCCC CGGGAGGGCG 1980
CGATCGGGAA TTC 1993

```

(2) INFORMATION FOR SEQ ID NO:39: 38 kD

(i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 374 amino acids
 (B) TYPE: amino acid
 (C) STRANDEDNESS:
 (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

```

Met Lys Ile Arg Leu His Thr Leu Leu Ala Val Leu Thr Ala Ala Pro
1          5          10          15
Leu Leu Leu Ala Ala Ala Gly Cys Gly Ser Lys Pro Pro Ser Gly Ser
20          25          30
Pro Glu Thr Gly Ala Gly Ala Gly Thr Val Ala Thr Thr Pro Ala Ser
35          40          45
Ser Pro Val Thr Leu Ala Glu Thr Gly Ser Thr Leu Leu Tyr Pro Leu
50          55          60
Phe Asn Leu Trp Gly Pro Ala Phe His Glu Arg Tyr Pro Asn Val Thr
65          70          75          80
Ile Thr Ala Gln Gly Thr Gly Ser Gly Ala Gly Ile Ala Gln Ala Ala
85          90          95
Ala Gly Thr Val Asn Ile Gly Ala Ser Asp Ala Tyr Leu Ser Glu Gly
100          105          110
Asp Met Ala Ala His Lys Gly Leu Met Asn Ile Ala Leu Ala Ile Ser
115          120          125
Ala Gln Gln Val Asn Tyr Asn Leu Pro Gly Val Ser Glu His Leu Lys
130          135          140
Leu Asn Gly Lys Val Leu Ala Ala Met Tyr Gln Gly Thr Ile Lys Thr
145          150          155          160
Trp Asp Asp Pro Gln Ile Ala Ala Leu Asn Pro Gly Val Asn Leu Pro
165          170          175
Gly Thr Ala Val Val Pro Leu His Arg Ser Asp Gly Ser Gly Asp Thr
180          185          190
Phe Leu Phe Thr Gln Tyr Leu Ser Lys Gln Asp Pro Glu Gly Trp Gly
195          200          205

```


Lys Ser Pro Gly Phe Gly Thr Thr Val Asp Phe Pro Ala Val Pro Gly
 210 215 220
 5 Ala Leu Gly Glu Asn Gly Asn Gly Gly Met Val Thr Gly Cys Ala Glu
 225 230 235 240
 Thr Pro Gly Cys Val Ala Tyr Ile Gly Ile Ser Phe Leu Asp Gln Ala
 245 250 255
 10 Ser Gln Arg Gly Leu Gly Glu Ala Gln Leu Gly Asn Ser Ser Gly Asn
 260 265 270
 Phe Leu Leu Pro Asp Ala Gln Ser Ile Gln Ala Ala Ala Gly Phe
 275 280 285
 15 Ala Ser Lys Thr Pro Ala Asn Gln Ala Ile Ser Met Ile Asp Gly Pro
 290 295 300
 20 Ala Pro Asp Gly Tyr Pro Ile Ile Asn Tyr Glu Tyr Ala Ile Val Asn
 305 310 315 320
 Asn Arg Gln Lys Asp Ala Ala Thr Ala Gln Thr Leu Gln Ala Phe Leu
 325 330 335
 25 His Trp Ala Ile Thr Asp Gly Asn Lys Ala Ser Phe Leu Asp Gln Val
 340 345 350
 His Phe Gln Pro Leu Pro Pro Ala Val Val Lys Leu Ser Asp Ala Leu
 355 360 365
 30 Ile Ala Thr Ile Ser Ser
 370
 35 (2) INFORMATION FOR SEQ ID NO:40: DPEP
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 999 base pairs
 (B) TYPE: nucleic acid
 40 (C) STRANDEDNESS: single
 (D) TOPOLOGY: linear
 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:
 45 ATGCATCACC ATCACCATCA CATGCATCAG GTGGACCCCA ACTTGACACG TCGCAAGGGA 60
 CGATTGGCGG CACTGGCTAT CGCGGCGATG GCCAGCGCCA GCCTGGTGAC CGTTGCGGTG 120
 CCCGCGACCG CCAACGCCGA TCCGGAGCCA GCGCCCCCGG TACCCACAAC GGCCGCCTCG 180
 CCGCCGTCGA CCGCTGCAGC GCCACCCGCA CCGCGACAC CTGTTGCCCC CCCACCACCG 240
 GCGCGCGCCA ACACGCCGAA TGCCAGCCG GCGGATCCCA ACGCAGCACC TCCGCCGGCC 300
 50 GACCCGAACG CACCGCCGCC ACCTGTCAAT GCCCAAACG CACCCCAACC TGTCGGATC 360
 GACAACCCGG TTGGAGGATT CAGCTTCGCG CTGCCTGCTG GCTGGGTGGA GTCTGACGCC 420
 GCCCCACTTC ACTACGGTTC AGCACTCCTC AGCAAAACCA CCGGGGACCC GCCATTTCCTC 480
 GGACAGCCGC CGCCGGTGCC CAATGACACC CGTATCGTGC TCGGCCGGCT AGACCAAAAG 540
 CTTTACGCCA GCGCCGAAGC CACCGACTCC AAGGCCGCGG CCCGGTTGGG CTCGGACATG 600
 55 GGTGAGTTCT ATATGCCCTA CCCGGGCACC CGGATCAACC AGGAAACCGT CTCGCTCGAC 660
 GCCAACGGGG TGTCTGGAAG CGCGTCGTAT TACGAAGTCA AGTTCAGCGA TCCGAGTAAG 720
 CCGAACGGCC AGATCTGGAC GGGCGTAATC GGCTCGCCCG CGGCGAACGC ACCGGACGCC 780
 GGGCCCCCTC AGCGCTGGTT TGTGGTATGG CTCGGGACCG CCAACAACCC GGTGGACAAG 840
 GCGCGGCCA AGGCGCTGGC CGAATCGATC CGGCCTTTGG TCGCCCCGCC GCGGGCGCCG 900
 60 GCACCGGCTC CTGCAGAGCC CGCTCCGGCG CCGGCGCCG CCGGGGAAGT CGCTCCTACC 960
 CCGACGACAC CGACACCGCA GCGGACCTTA CCGGCCTGA 999

65 (2) INFORMATION FOR SEQ ID NO:41: DPEP
 (i) SEQUENCE CHARACTERISTICS:
 (A) LENGTH: 332 amino acids
 (B) TYPE: amino acid

(C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

5 Met His His His His His His Met His Gln Val Asp Pro Asn Leu Thr
1 5 10 15
Arg Arg Lys Gly Arg Leu Ala Ala Leu Ala Ile Ala Ala Met Ala Ser
20 25 30
10 Ala Ser Leu Val Thr Val Ala Val Pro Ala Thr Ala Asn Ala Asp Pro
35 40 45
Glu Pro Ala Pro Pro Val Pro Thr Thr Ala Ala Ser Pro Pro Ser Thr
50 55 60
15 Ala Ala Ala Pro Pro Ala Pro Ala Thr Pro Val Ala Pro Pro Pro Pro
65 70 75 80
Ala Ala Ala Asn Thr Pro Asn Ala Gln Pro Gly Asp Pro Asn Ala Ala
85 90 95
Pro Pro Pro Ala Asp Pro Asn Ala Pro Pro Pro Pro Val Ile Ala Pro
100 105 110
20 Asn Ala Pro Gln Pro Val Arg Ile Asp Asn Pro Val Gly Phe Ser
115 120 125
Phe Ala Leu Pro Ala Gly Trp Val Glu Ser Asp Ala Ala His Phe Asp
130 135 140
25 Tyr Gly Ser Ala Leu Leu Ser Lys Thr Thr Gly Asp Pro Pro Phe Pro
145 150 155 160
Gly Gln Pro Pro Pro Val Ala Asn Asp Thr Arg Ile Val Leu Gly Arg
165 170 175
Leu Asp Gln Lys Leu Tyr Ala Ser Ala Glu Ala Thr Asp Ser Lys Ala
180 185 190
30 Ala Ala Arg Leu Gly Ser Asp Met Gly Glu Phe Tyr Met Pro Tyr Pro
195 200 205
Gly Thr Arg Ile Asn Gln Glu Thr Val Ser Leu Asp Ala Asn Gly Val
210 215 220
35 Ser Gly Ser Ala Ser Tyr Tyr Glu Val Lys Phe Ser Asp Pro Ser Lys
225 230 235 240
Pro Asn Gly Gln Ile Trp Thr Gly Val Ile Gly Ser Pro Ala Ala Asn
245 250 255
Ala Pro Asp Ala Gly Pro Pro Gln Arg Trp Phe Val Val Trp Leu Gly
260 265 270
40 Thr Ala Asn Asn Pro Val Asp Lys Gly Ala Ala Lys Ala Leu Ala Glu
275 280 285
Ser Ile Arg Pro Leu Val Ala Pro Pro Pro Ala Pro Ala Pro Ala Pro
290 295 300
45 Ala Glu Pro Ala Pro Ala Pro Ala Pro Ala Gly Glu Val Ala Pro Thr
305 310 315 320
Pro Thr Thr Pro Thr Pro Gln Arg Thr Leu Pro Ala
325 330

50 (2) INFORMATION FOR SEQ ID NO:42: TbH4

(i) SEQUENCE CHARACTERISTICS:
(A) LENGTH: 702 base pairs
(B) TYPE: nucleic acid
55 (C) STRANDEDNESS: single
(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

60 CGGCACGAGG ATCGGTACCC CGCGGCATCG GCAGCTGCCG ATTCGCCGGG TTTCCCCACC 60
CGAGGAAAGC CGCTACCAGA TGGCGCTGCC GAAGTAGGGC GATCCGTTCG CGATGCCGGC 120
ATGACCGGGC GGCATCAAAAT TAGTGCAGGA ACCTTTCAGT TTAGCGACGA TAATGGCTAT 180
AGCACTAAGG AGGATGATCC GATATGACGC AGTCGCAGAC CGTGACGGTG GATCAGCAAG 240
AGATTTTGAA CAGGGCCAAC GAGGTGGAGG CCCCAGTGGC GGACCCACCG ACTGATGTCC 300
65 CCATCACACC GTGCGAACTC ACGGNGGNTA AAAACGCCGC CCAACAGNTG GTNTGTCCG 360
CCGACAACAT GCGGAATAC CTGGCGGCCG GTGCCAAGA GCGGCAGCGT CTGGCGACCT 420
CGCTGCGCAA CGCGGCCAAG GNGTATGGCG AGGTTGATGA GGAGGCTGCG ACCGCGCTGG 480
ACAACGACGG CGAAGGAAC GTGCAGGCAG AATCGGCCG GGCCGTCGGA GGGGACAGTT 540

CGGCCGAAC T AACCGATACG CCGAGGGTGG CCACGGCCGG TGAACCCAAC TTCATGGATC 600
TCAAAGAAGC GGCAAGGAAG CTCGAAACGG GCGACCAAGG CGCATCGCTC GCGCACTGNG 660
GGGATGGGTG GAACACTTNC ACCCTGACGC TGCAAGGCGA CG 702

5

(2) INFORMATION FOR SEQ ID NO:43: TbH4

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 286 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

Gly Asp Ser Phe Trp Ala Ala Ala Asp Gln Met Ala Arg Gly Phe Val
1 5 10 15
Leu Gly Ala Thr Ala Gly Arg Thr Thr Leu Thr Gly Glu Gly Leu Gln
20 25 30
His Ala Asp Gly His Ser Leu Leu Asp Ala Thr Asn Pro Ala Val
35 40 45
Val Ala Tyr Asp Pro Ala Phe Ala Tyr Glu Ile Gly Tyr Ile Xaa Glu
50 55 60
Ser Gly Leu Ala Arg Met Cys Gly Glu Asn Pro Glu Asn Ile Phe Phe
65 70 75 80
Tyr Ile Thr Val Tyr Asn Glu Pro Tyr Val Gln Pro Pro Glu Pro Glu
85 90 95
Asn Phe Asp Pro Glu Gly Val Leu Gly Gly Ile Tyr Arg Tyr His Ala
100 105 110
Ala Thr Glu Gln Arg Thr Asn Lys Xaa Gln Ile Leu Ala Ser Gly Val
115 120 125
Ala Met Pro Ala Ala Leu Arg Ala Ala Gln Met Leu Ala Ala Glu Trp
130 135 140
Asp Val Ala Ala Asp Val Trp Ser Val Thr Ser Trp Gly Glu Leu Asn
145 150 155 160
Arg Asp Gly Val Val Ile Glu Thr Glu Lys Leu Arg His Pro Asp Arg
165 170 175
Pro Ala Gly Val Pro Tyr Val Thr Arg Ala Leu Glu Asn Ala Arg Gly
180 185 190
Pro Val Ile Ala Val Ser Asp Trp Met Arg Ala Val Pro Glu Gln Ile
195 200 205
Arg Pro Trp Val Pro Gly Thr Tyr Leu Thr Leu Gly Thr Asp Gly Phe
210 215 220
Gly Phe Ser Asp Thr Arg Pro Ala Gly Arg Arg Tyr Phe Asn Thr Asp
225 230 235 240
Ala Glu Ser Gln Val Gly Arg Gly Phe Gly Arg Gly Trp Pro Gly Arg
245 250 255
Arg Val Asn Ile Asp Pro Phe Gly Ala Gly Arg Gly Pro Pro Ala Gln
260 265 270
Leu Pro Gly Phe Asp Glu Gly Gly Leu Arg Pro Xaa Lys
275 280 285

(2) INFORMATION FOR SEQ ID NO:44: DPPD

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 339 base pairs

(B) TYPE: nucleic acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: Genomic DNA

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

ATGAAGTTGA AGTTTGCTCG CCTGAGTACT GCGATACTGG GTTGTGCAGC GGCGCTTGTG 60
TTTCCTGCCT CGGTTGCCAG CGCAGATCCA CCTGACCCGC ATCAGCCGGA CATGACGAAA 120
GGCTATTGCC CGGGTGGCCG ATGGGGTTTT GGCGACTTGG CCGTGTGCGA CGGCGAGAAG 180

TACCCCGACG GCTCGTTTTG GCACCAAGTGG ATGCAAACGT GGTTTACCGG CCCACAGTTT 240
TACTTCGATT GTGTCAGCGG CGGTGAGCCC CTCCCCGGCC CGCCGCCACC GGGTGGTTGC 300
GGTGGGGCAA TTCCGTCCGA GCAGCCCAAC GCTCCCTGA 339

5

(2) INFORMATION FOR SEQ ID NO:45: DPPD

(i) SEQUENCE CHARACTERISTICS:

(A) LENGTH: 112 amino acids

(B) TYPE: amino acid

(C) STRANDEDNESS: single

(D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

Met Lys Leu Lys Phe Ala Arg Leu Ser Thr Ala Ile Leu Gly Cys Ala
1 5 10 15
Ala Ala Leu Val Phe Pro Ala Ser Val Ala Ser Ala Asp Pro Pro Asp
20 25 30
Pro His Gln Pro Asp Met Thr Lys Gly Tyr Cys Pro Gly Gly Arg Trp
35 40 45
Gly Phe Gly Asp Leu Ala Val Cys Asp Gly Glu Lys Tyr Pro Asp Gly
50 55 60
Ser Phe Trp His Gln Trp Met Gln Thr Trp Phe Thr Gly Pro Gln Phe
65 70 75 80
Tyr Phe Asp Cys Val Ser Gly Gly Glu Pro Leu Pro Gly Pro Pro Pro
85 90 95
Pro Gly Gly Cys Gly Gly Ala Ile Pro Ser Glu Gln Pro Asn Ala Pro
100 105 110

<210> SEQ ID NO:46

<211> 921

<212> DNA

<213> Artificial Sequence

<223> Description of Artificial Sequence:tri-fusion
protein DPV-MTI-MSL (designated Mtb31f)

<222> (1)..(900)

cat atg cat cac cat cac cat cac gat ccc gtg gac gcg gtc att aac 48
His Met His His His His His His Asp Pro Val Asp Ala Val Ile Asn
1 5 10 15

acc acc tgc aat tac ggg cag gta gta gct gcg ctc aac gcg acg gat 96
Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp
20 25 30

ccg ggg gct gcc gca cag ttc aac gcc tca ccg gtg gcg cag tcc tat 144
Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr
35 40 45

ttg cgc aat ttc ctc gcc gca ccg cca cct cag cgc gct gcc atg gcc 192
Leu Arg Asn Phe Leu Ala Ala Pro Pro Pro Gln Arg Ala Ala Met Ala
50 55 60

gcg caa ttg caa gct gtg ccg ggg gcg gca cag tac atc ggc ctt gtc 240
Ala Gln Leu Gln Ala Val Pro Gly Ala Ala Gln Tyr Ile Gly Leu Val
65 70 75 80

gag tgc gtt gcc ggc tcc tgc aac aac tat gag ctc atg acg att aat 288
Glu Ser Val Ala Gly Ser Cys Asn Asn Tyr Glu Leu Met Thr Ile Asn
85 90 95

tac cag ttc ggg gac gtc gac gct cat ggc gcc atg atc cgc gct cag 336
Tyr Gln Phe Gly Asp Val Asp Ala His Gly Ala Met Ile Arg Ala Gln
100 105 110

	gcg gcg tcg ctt gag gcg gag cat cag gcc atc gtt cgt gat gtg ttg	384
	Ala Ala Ser Leu Glu Ala Glu His Gln Ala Ile Val Arg Asp Val Leu	
	115 120 125	
5	gcc gcg ggt gac ttt tgg ggc ggc gcc ggt tcg gtg gct tgc cag gag	432
	Ala Ala Gly Asp Phe Trp Gly Gly Ala Gly Ser Val Ala Cys Gln Glu	
	130 135 140	
10	ttc att acc cag ttg ggc cgt aac ttc cag gtg atc tac gag cag gcc	480
	Phe Ile Thr Gln Leu Gly Arg Asn Phe Gln Val Ile Tyr Glu Gln Ala	
	145 150 155 160	
15	aac gcc cac ggg cag aag gtg cag gct gcc ggc aac aac atg gcg caa	528
	Asn Ala His Gly Gln Lys Val Gln Ala Ala Gly Asn Asn Met Ala Gln	
	165 170 175	
20	acc gac agc gcc gtc ggc tcc agc tgg gcc act agt atg agc ctt ttg	576
	Thr Asp Ser Ala Val Gly Ser Ser Trp Ala Thr Ser Met Ser Leu Leu	
	180 185 190	
25	gat gct cat atc cca cag ttg gtg gcc tcc cag tcg gcg ttt gcc gcc	624
	Asp Ala His Ile Pro Gln Leu Val Ala Ser Gln Ser Ala Phe Ala Ala	
	195 200 205	
30	aag gcg ggg ctg atg cgg cac acg atc ggt cag gcc gag cag gcg gcg	672
	Lys Ala Gly Leu Met Arg His Thr Ile Gly Gln Ala Glu Gln Ala Ala	
	210 215 220	
35	atg tcg gct cag gcg ttt cac cag ggg gag tcg tcg gcg gcg ttt cag	720
	Met Ser Ala Gln Ala Phe His Gln Gly Glu Ser Ser Ala Ala Phe Gln	
	225 230 235 240	
40	gcc gcc cat gcc cgg ttt gtg gcg gcg gcc gcc aaa gtc aac acc ttg	768
	Ala Ala His Ala Arg Phe Val Ala Ala Ala Lys Val Asn Thr Leu	
	245 250 255	
45	ttg gat gtc gcg cag gcg aat ctg ggt gag gcc gcc ggt acc tat gtg	816
	Leu Asp Val Ala Gln Ala Asn Leu Gly Glu Ala Ala Gly Thr Tyr Val	
	260 265 270	
50	gcc gcc gat gct gcg gcc gcg tcg acc tat acc ggg ttc gat atc cat	864
	Ala Ala Asp Ala Ala Ala Ala Ser Thr Tyr Thr Gly Phe Asp Ile His	
	275 280 285	
55	cac act ggc ggc cgc tcg agc aga tcc ggc tgc taacaagacc cgaaaggaag	917
	His Thr Gly Gly Arg Ser Ser Arg Ser Gly Cys	
	290 295	
60	ctga	921
55	<210> SEQ ID NO:47	
	<211> 299	
	<212> PRT	
	<213> Artificial Sequence	
	<223> Description of Artificial Sequence:tri-fusion	
	protein DPV-MTI-MSL (designated Mtb31f)	
60	His Met His His His His His His Asp Pro Val Asp Ala Val Ile Asn	
	1 5 10 15	
65	Thr Thr Cys Asn Tyr Gly Gln Val Val Ala Ala Leu Asn Ala Thr Asp	
	20 25 30	
	Pro Gly Ala Ala Ala Gln Phe Asn Ala Ser Pro Val Ala Gln Ser Tyr	
	35 40 45	

5	ttg	cgc	aat	ttc	ctc	gcc	gca	ccg	cca	cct	cag	cgc	gct	gcc	atg	gcc	192
	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro	Gln	Arg	Ala	Ala	Met	Ala	
	50						55					60					
	gcg	caa	ttg	caa	gct	gtg	ccg	ggg	gcg	gca	cag	tac	atc	ggc	ctt	gtc	240
	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala	Gln	Tyr	Ile	Gly	Leu	Val	
	65					70					75					80	
10	gag	tcg	gtt	gcc	ggc	tcc	tgc	aac	aac	tat	gag	ctc	atg	acg	att	aat	288
	Glu	Ser	Val	Ala	Gly	Ser	Cys	Asn	Asn	Tyr	Glu	Leu	Met	Thr	Ile	Asn	
					85					90					95		
15	tac	cag	ttc	ggg	gac	gtc	gac	gct	cat	ggc	gcc	atg	atc	cgc	gct	cag	336
	Tyr	Gln	Phe	Gly	Asp	Val	Asp	Ala	His	Gly	Ala	Met	Ile	Arg	Ala	Gln	
				100					105					110			
20	gcg	gcg	tcg	ctt	gag	gcg	gag	cat	cag	gcc	atc	gtt	cgt	gat	gtg	ttg	384
	Ala	Ala	Ser	Leu	Glu	Ala	Glu	His	Gln	Ala	Ile	Val	Arg	Asp	Val	Leu	
			115					120					125				
25	gcc	gcg	ggg	gac	ttt	tgg	ggc	ggc	gcc	ggt	tcg	gtg	gct	tgc	cag	gag	432
	Ala	Ala	Gly	Asp	Phe	Trp	Gly	Gly	Ala	Gly	Ser	Val	Ala	Cys	Gln	Glu	
			130				135					140					
30	ttc	att	acc	cag	ttg	ggc	cgt	aac	ttc	cag	gtg	atc	tac	gag	cag	gcc	480
	Phe	Ile	Thr	Gln	Leu	Gly	Arg	Asn	Phe	Gln	Val	Ile	Tyr	Glu	Gln	Ala	
					150						155					160	
35	aac	gcc	cac	ggg	cag	aag	gtg	cag	gct	gcc	ggc	aac	aac	atg	gcg	caa	528
	Asn	Ala	His	Gly	Gln	Lys	Val	Gln	Ala	Ala	Gly	Asn	Asn	Met	Ala	Gln	
					165					170				175			
40	acc	gac	agc	gcc	gtc	ggc	tcc	agc	tgg	gcc	act	agt	atg	agc	ctt	ttg	576
	Thr	Asp	Ser	Ala	Val	Gly	Ser	Ser	Trp	Ala	Thr	Ser	Met	Ser	Leu	Leu	
				180					185					190			
45	gat	gct	cat	atc	cca	cag	ttg	gtg	gcc	tcc	cag	tcg	gcg	ttt	gcc	gcc	624
	Asp	Ala	His	Ile	Pro	Gln	Leu	Val	Ala	Ser	Gln	Ser	Ala	Phe	Ala	Ala	
				195				200					205				
50	aag	gcg	ggg	ctg	atg	cgg	cac	acg	atc	ggt	cag	gcc	gag	cag	gcg	gcg	672
	Lys	Ala	Gly	Leu	Met	Arg	His	Thr	Ile	Gly	Gln	Ala	Glu	Gln	Ala	Ala	
			210				215					220					
55	atg	tcg	gct	cag	gcg	ttt	cac	cag	ggg	gag	tcg	tcg	gcg	gcg	ttt	cag	720
	Met	Ser	Ala	Gln	Ala	Phe	His	Gln	Gly	Glu	Ser	Ser	Ala	Ala	Phe	Gln	
						230					235					240	
60	gcc	gcc	cat	gcc	cgg	ttt	gtg	gcg	gcg	gcc	gcc	aaa	gtc	aac	acc	ttg	768
	Ala	Ala	His	Ala	Arg	Phe	Val	Ala	Ala	Ala	Ala	Lys	Val	Asn	Thr	Leu	

5	gtg gcc gcg gag ttg act tcc gcc gcg gtc tcg tat gga tcg gtg gtg 1008 Val Ala Ala Glu Leu Thr Ser Ala Ala Val Ser Tyr Gly Ser Val Val 325 330 335
10	tcg acg ctg atc gtt gag ccg tgg atg ggg ccg gcg gcg gcc gcg atg 1056 Ser Thr Leu Ile Val Glu Pro Trp Met Gly Pro Ala Ala Ala Ala Met 340 345 350
15	gcg gcc gcg gca acg ccg tat gtg ggg tgg ctg gcc gcc acg gcg gcg 1104 Ala Ala Ala Ala Thr Pro Tyr Val Gly Trp Leu Ala Ala Thr Ala Ala 355 360 365
20	ctg gcg aag gag acg gcc aca cag gcg agg gca gcg gcg gaa gcg ttt 1152 Leu Ala Lys Glu Thr Ala Thr Gln Ala Arg Ala Ala Ala Glu Ala Phe 370 375 380
25	ggg acg gcg ttc gcg atg acg gtg cca cca tcc ctc gtc gcg gcc aac 1200 Gly Thr Ala Phe Ala Met Thr Val Pro Pro Ser Leu Val Ala Ala Asn 385 390 395 400
30	cgc agc cgg ttg atg tcg ctg gtc gcg gcg aac att ctg ggg caa aac 1248 Arg Ser Arg Leu Met Ser Leu Val Ala Ala Asn Ile Leu Gly Gln Asn 405 410 415
35	agt gcg gcg atc gcg gct acc cag gcc gag tat gcc gaa atg tgg gcc 1296 Ser Ala Ala Ile Ala Ala Thr Gln Ala Glu Tyr Ala Glu Met Trp Ala 420 425 430
40	caa gac gct gcc gtg atg tac agc tat gag ggg gca tct gcg gcc gcg 1344 Gln Asp Ala Ala Val Met Tyr Ser Tyr Glu Gly Ala Ser Ala Ala Ala 435 440 445
45	tcg gcg ttg ccg ccg ttc act cca ccc gtg caa ggc acc ggc ccg gcc 1392 Ser Ala Leu Pro Pro Phe Thr Pro Pro Val Gln Gly Thr Gly Pro Ala 450 455 460
50	ggg ccc gcg gcc gca gcc gcg gcg acc caa gcc gcc ggt gcg ggc gcc 1440 Gly Pro Ala Ala Ala Ala Ala Thr Gln Ala Ala Gly Ala Gly Ala 465 470 475 480
55	gtt gcg gat gca cag gcg aca ctg gcc cag ctg ccc ccg ggg atc ctg 1488 Val Ala Asp Ala Gln Ala Thr Leu Ala Gln Leu Pro Pro Gly Ile Leu 485 490 495
60	agc gac att ctg tcc gca ttg gcc gcc aac gct gat ccg ctg aca tcg 1536 Ser Asp Ile Leu Ser Ala Leu Ala Ala Asn Ala Asp Pro Leu Thr Ser 500 505 510
65	gga ctg ttg ggg atc gcg tcg acc ctc aac ccg caa gtc gga tcc gct 1584 Gly Leu Leu Gly Ile Ala Ser Thr Leu Asn Pro Gln Val Gly Ser Ala 515 520 525
70	cag ccg ata gtg atc ccc acc ccg ata ggg gaa ttg gac gtg atc gcg 1632 Gln Pro Ile Val Ile Pro Thr Pro Ile Gly Glu Leu Asp Val Ile Ala 530 535 540
75	ctc tac att gca tcc atc gcg acc ggc agc att gcg ctc gcg atc acg 1680 Leu Tyr Ile Ala Ser Ile Ala Thr Gly Ser Ile Ala Leu Ala Ile Thr 545 550 555 560
80	aac acg gcc aga ccc tgg cac atc ggc cta tac ggg aac gcc ggc ggg 1728 Asn Thr Ala Arg Pro Trp His Ile Gly Leu Tyr Gly Asn Ala Gly Gly 565 570 575
85	ctg gga ccg acg cag ggc cat cca ctg agt tcg gcg acc gac gag ccg 1776 Leu Gly Pro Thr Gln Gly His Pro Leu Ser Ser Ala Thr Asp Glu Pro 580 585 590

	gag	ccg	cac	tgg	ggc	ccc	ttc	ggg	ggc	gcg	gcg	ccg	gtg	tcc	gcg	ggc	1824
	Glu	Pro	His	Trp	Gly	Pro	Phe	Gly	Gly	Ala	Ala	Pro	Val	Ser	Ala	Gly	
			595					600					605				
5	gtc	ggc	cac	gca	gca	tta	gtc	gga	gcg	ttg	tcg	gtg	ccg	cac	agc	tgg	1872
	Val	Gly	His	Ala	Ala	Leu	Val	Gly	Ala	Leu	Ser	Val	Pro	His	Ser	Trp	
		610					615					620					
10	acc	acg	gcc	gcc	ccg	gag	atc	cag	ctc	gcc	gtt	cag	gca	aca	ccc	acc	1920
	Thr	Thr	Ala	Ala	Pro	Glu	Ile	Gln	Leu	Ala	Val	Gln	Ala	Thr	Pro	Thr	
						630						635				640	
15	ttc	agc	tcc	agc	gcc	ggc	gcc	gac	ccg	acg	gcc	cta	aac	ggg	atg	ccg	1968
	Phe	Ser	Ser	Ser	Ala	Gly	Ala	Asp	Pro	Thr	Ala	Leu	Asn	Gly	Met	Pro	
					645						650				655		
20	gca	ggc	ctg	ctc	agc	ggg	atg	gct	ttg	gcg	agc	ctg	gcc	gca	cgc	ggc	2016
	Ala	Gly	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Ser	Leu	Ala	Ala	Arg	Gly	
				660					665					670			
25	acg	acg	ggc	ggc	ggc	ggc	acc	cgt	agc	ggc	acc	agc	act	gac	ggc	caa	2064
	Thr	Thr	Gly	Gly	Gly	Gly	Thr	Arg	Ser	Gly	Thr	Ser	Thr	Asp	Gly	Gln	
			675					680					685				
30	gag	gac	ggc	cgc	aaa	ccc	ccg	gta	gtt	gtg	att	aga	gag	cag	ccg	ccg	2112
	Glu	Asp	Gly	Arg	Lys	Pro	Pro	Val	Val	Val	Ile	Arg	Glu	Gln	Pro	Pro	
		690					695					700					
35	ccc	gga	aac	ccc	ccg	cgg	taagatttct	aaatccatca	cactggcggc	cgctcgag							2168
	Pro	Gly	Asn	Pro	Pro	Arg											
	705					710											
40	<210>	SEQ	ID	NO:49													
	<211>	710															
	<212>	PRT															
	<213>	Artificial	Sequence														
	<223>	Description of Artificial	Sequence:tetra-fusion														
		protein DPV-MTI-MSL-MTCC2	(designated Mtb71f)														
45	His	Met	His	His	His	His	His	His	Asp	Pro	Val	Asp	Ala	Val	Ile	Asn	
	1				5					10					15		
50	Thr	Thr	Cys	Asn	Tyr	Gly	Gln	Val	Val	Ala	Ala	Leu	Asn	Ala	Thr	Asp	
				20					25					30			
55	Pro	Gly	Ala	Ala	Ala	Gln	Phe	Asn	Ala	Ser	Pro	Val	Ala	Gln	Ser	Tyr	
			35					40					45				
60	Leu	Arg	Asn	Phe	Leu	Ala	Ala	Pro	Pro	Pro	Gln	Arg	Ala	Ala	Met	Ala	
		50				55						60					
65	Ala	Gln	Leu	Gln	Ala	Val	Pro	Gly	Ala	Ala	Gln</						

	Gly	Leu	Leu	Gly	Ile	Ala	Ser	Thr	Leu	Asn	Pro	Gln	Val	Gly	Ser	Ala	
		515						520					525				
5	Gln	Pro	Ile	Val	Ile	Pro	Thr	Pro	Ile	Gly	Glu	Leu	Asp	Val	Ile	Ala	
		530					535					540					
	Leu	Tyr	Ile	Ala	Ser	Ile	Ala	Thr	Gly	Ser	Ile	Ala	Leu	Ala	Ile	Thr	
	545					550					555					560	
10	Asn	Thr	Ala	Arg	Pro	Trp	His	Ile	Gly	Leu	Tyr	Gly	Asn	Ala	Gly	Gly	
					565					570					575		
	Leu	Gly	Pro	Thr	Gln	Gly	His	Pro	Leu	Ser	Ser	Ala	Thr	Asp	Glu	Pro	
15				580					585					590			
	Glu	Pro	His	Trp	Gly	Pro	Phe	Gly	Gly	Ala	Ala	Pro	Val	Ser	Ala	Gly	
			595					600					605				
20	Val	Gly	His	Ala	Ala	Leu	Val	Gly	Ala	Leu	Ser	Val	Pro	His	Ser	Trp	
		610					615					620					
	Thr	Thr	Ala	Ala	Pro	Glu	Ile	Gln	Leu	Ala	Val	Gln	Ala	Thr	Pro	Thr	
	625					630					635					640	
25	Phe	Ser	Ser	Ser	Ala	Gly	Ala	Asp	Pro	Thr	Ala	Leu	Asn	Gly	Met	Pro	
					645					650					655		
	Ala	Gly	Leu	Leu	Ser	Gly	Met	Ala	Leu	Ala	Ser	Leu	Ala	Ala	Arg	Gly	
30				660					665					670			
	Thr	Thr	Gly	Gly	Gly	Gly	Thr	Arg	Ser	Gly	Thr	Ser	Thr	Asp	Gly	Gln	
			675					680						685			
35	Glu	Asp	Gly	Arg	Lys	Pro	Pro	Val	Val	Val	Ile	Arg	Glu	Gln	Pro	Pro	
		690					695					700					
	Pro	Gly	Asn	Pro	Pro	Arg											
40		705				710											